

FIG. 1A

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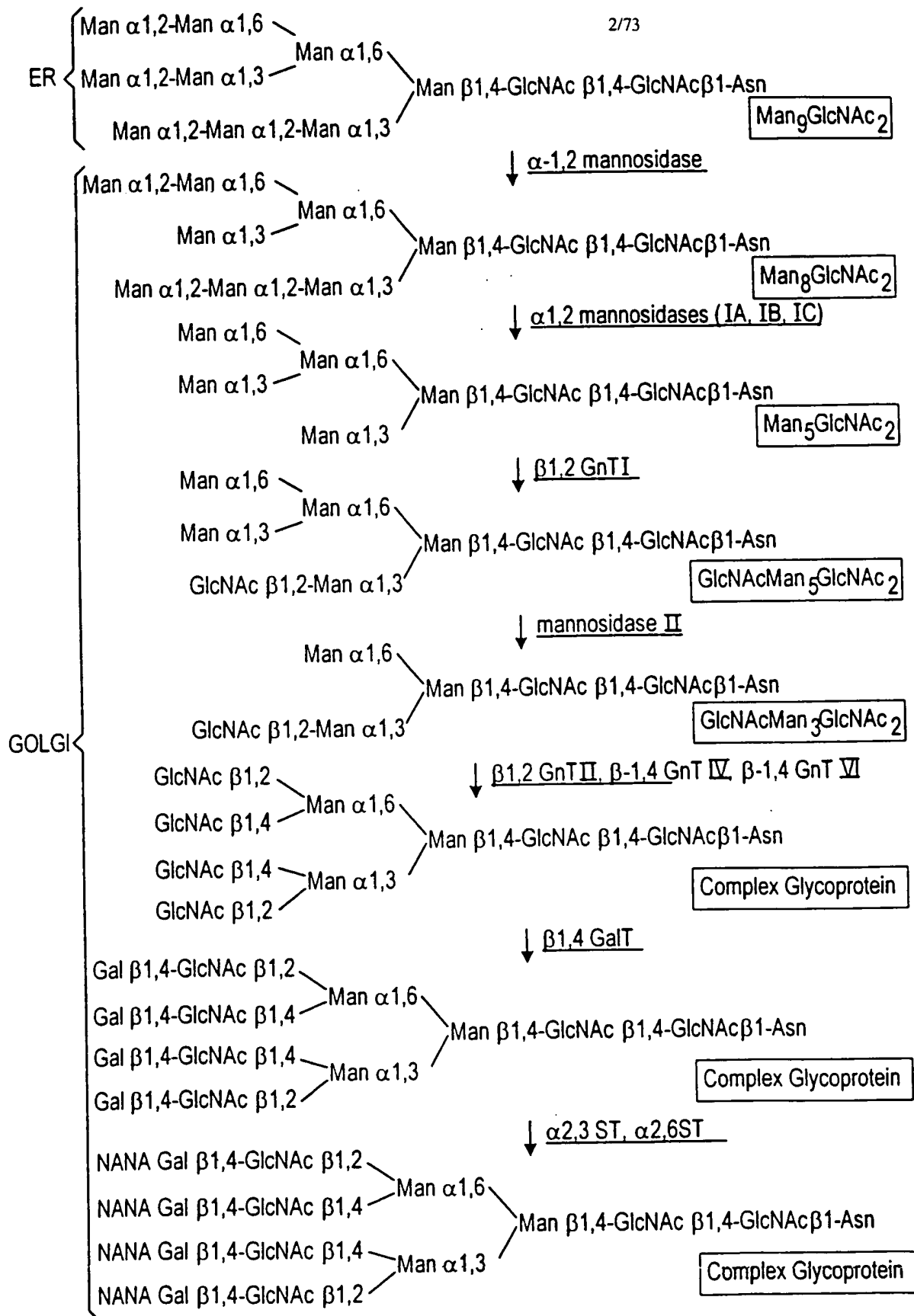


FIG. 1B

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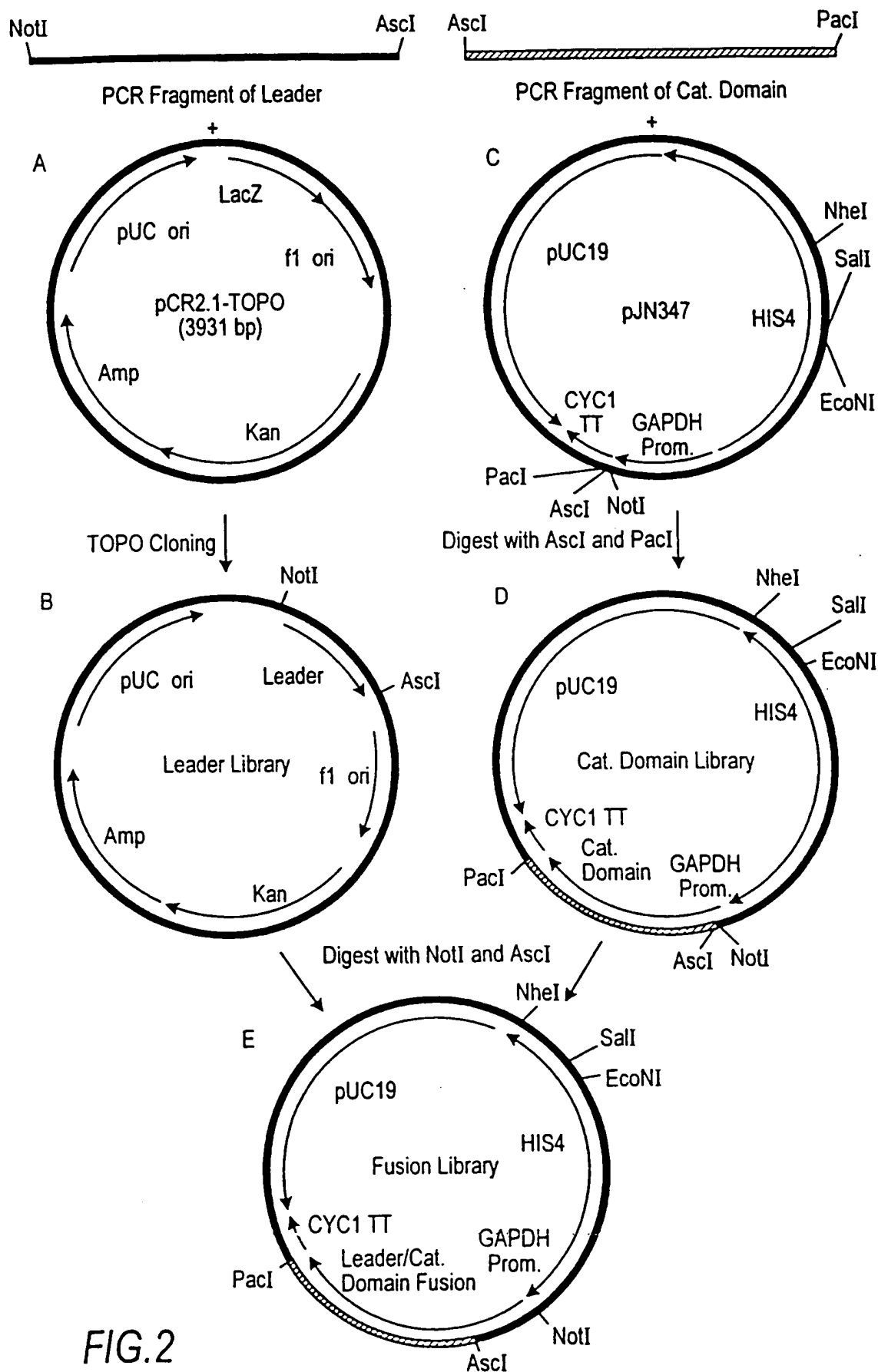


FIG.2

M. musculus alpha-1,2-mannosidase IA open reading frame. The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.

```

1  atgcccgtggggcctgttgcgcgtcttccagtagcccttggggggggccttggcagtgggccttggggggccttggcggcgggaggaagg
1▶ M P V G G L L P L F S S P G G G L G S G L G G L G G L G G R K G
97  tctgccccgcgtgcttccgcctcaccgagaagtctcgtgctggtgttcagcgccttcacagctotgcttgcggggcaatc
33▶ S G P A A F R L T E K F V L L V F S A F I T L C F G A I
184  ttcttctgctgctgactctctccaaagctgctcagcgggtcctgttccactccaaacctgcttgcagccgcggcggagcacaagcccggtcgcg
62▶ F F L P D S S K L L S G V L F H S N P A L Q P P A E H K P G L
      d65 primer
278  gggcgctgaggatgcccgcgagggggagagtcctccggcaccgcgagggaaggcgccctgggagcctggagctggactggagagacaacttagcca
93▶ G A R A E D A E G R V R H R E E G A P G D P G A G L E D N L A
      d105 primer
374  ggatccgcgaaacacgagcgggctctcagggaagcccaaggagaccctgcagaagctccggaggagatccaaagagacattctgtggagaagg
125▶ R I R E N H E R A L R E A K E T L Q K L P E I Q R D I L L E K
470  aaaaggtggcccgaccagctgcgtgacaaggatctgtttagggttgcaccaagtggtgacttctcccccccgctcggggttagagaaccggggagc
157▶ E K V A Q D Q L R D K D L F R G L P K V D F L P P V G V E N R E
      d187 primer
566  ccgctgacgcccaccatccgtgagaagaggggcaagatcaagagatgatgacccatgcttggaaataattataaacgctatgcgtggggc
189▶ P A D A T I R E K R A K I K E M M T H A W N N Y K R Y A W G
  
```

FIG. 3

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655 ttgaacgaactgaacacctatataaaagaaggccattcaagcagttgtttggcaacatcaaaaggagctacaatagtagatg
 219▶ L N E L K P I S K E G H S S L F G N I K G A T I V D
 737 ccctggataccctttcattatggcctgaagactgaattcaagaagctaaatcggtgattataaaaaatatttagatttttaa
 246▶ A L D T L F I M G M K T E F Q E A K S W I K K Y L D F N
 819 tgtgaatgctgaagtctctgttttgaagtcaacatacgtcttgcgttggtgactgctgcagcctactatttgcgcggagag
 273▶ V N A E V S V F E V N I R F V G G L L S A Y Y L S G E
 901 gagatatctgaagaagcagtggaacttgggtataaattgctacctgcattctactcctctctggaataccttgggcat
 301▶ E I F R K K A V E L G V K L L P A F H T P S G I P W A
 983 tgctgaatatgaagaagtgggacgtggcggaactggccctggccctctggaggcagcagtagtccctggccgaatttggaaactct
 328▶ L L N M K S G I G R N W P W A S G G S S I L A E F G T L
 1065 gcatttagagtttatgcactgttccacttatcaggagacccagctcttggccgaagaaggttatgaaaatttcgaacagtggtg
 355▶ H L E F M H L S H L S G D P V F A E K V M K I R T V L
 1147 acaaaactggacaaaccagaaggcctttatcctaactatctgaaccccccagtagtgacacagtggtgggtcaacatcatgtgtcgg
 383▶ N K L D K P E G L Y P N Y L N P S S G Q W G Q H H V S
 1229 ttggaggacttgagacagcttttatgaatatattgtcttaaggcgtggttaattgtctgacaaagacagatctcgaagcgaagaa
 410▶ V G G L G D S F Y E Y L L K A W L M S D K T D L E A K K
 1311 gatgtatttgatgctgttcaggccatcgagactcaacttgatccgcaagtcaagtggtgggactaacgtacatcgacagtggtg
 437▶ M Y F D A V Q A I E T H L I R K S S G G L T Y I A E W
 1393 aaggggggcctcctggaacacaaagatggggccacctgagctgtttgcaggaggcagtagtggcacttggcagtggtggcagatggagctc
 465▶ K G G L L E H K M G H L T C F A G G M F A L G A D G A
 1475 cggaagcccgcccaacactaccttgaaactcgagctgaaattggcccgcaattgctcatgaattcttataatcgtacatagt
 492▶ P E A R A Q H Y L E L G A E I A R T C H E S Y N R T Y V
 1557 gaagtgggaccggaagcgtttcgtattgttgccggtgtggaagctattggccacgaggcgaataatgaagaatgaataatctta
 519▶ K L G P E A F R F D G G V E A I A T R Q N E K Y Y I L
 1639 cgcccgagggtcatcgagacatacatgtacatgtggcgactgactcaacaccccaagtaacaggaacctgggctgggaagccg
 547▶ R P E V I E T Y M Y M W R L T H D P K Y R T W A W E A
 1721 tggaggctctagaagtcaactgcagagtgaaacggaggctactcaggcttaagggtattgattacattgcccgtgagagttatga
 574▶ V E A L E S H C R V N G G Y S G L R D V Y I A R E S Y D
 1803 cgatgtccagcaagttcttctcctggcagacactgaagtattgttacttgatatttccgattgacacatttcttccacta
 601▶ D V Q Q S F F L A E T L K Y L I F S D D L L P L
 1885 gaacactggtatcttcaacacccagggtctcatcttccctatactcctgtaacagaagaaggaattgattggcaagagaatga
 629▶ E H W I F N T E A H P F P I L R E Q K K E I D G K E K

FIG. 3 CONT

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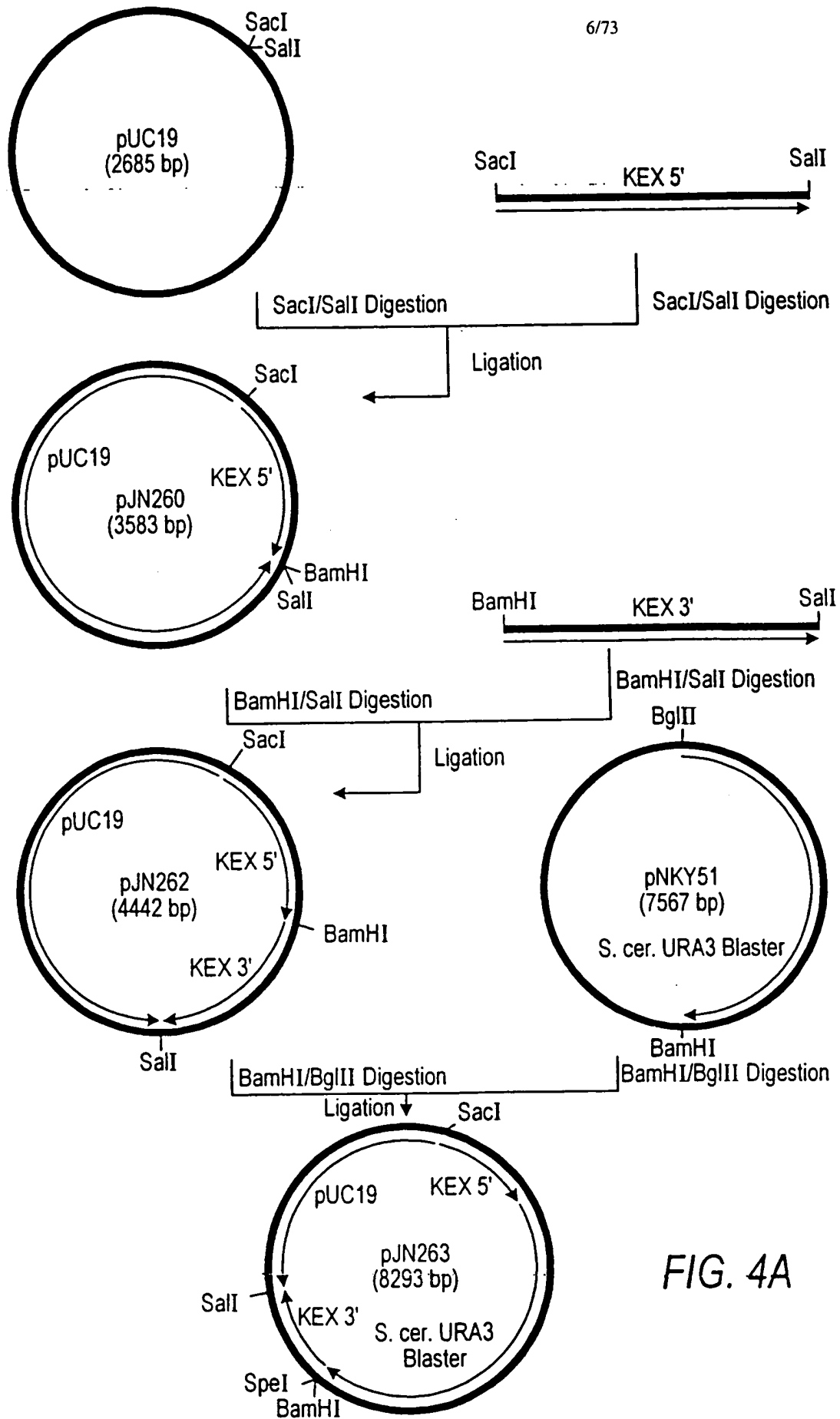


FIG. 4A

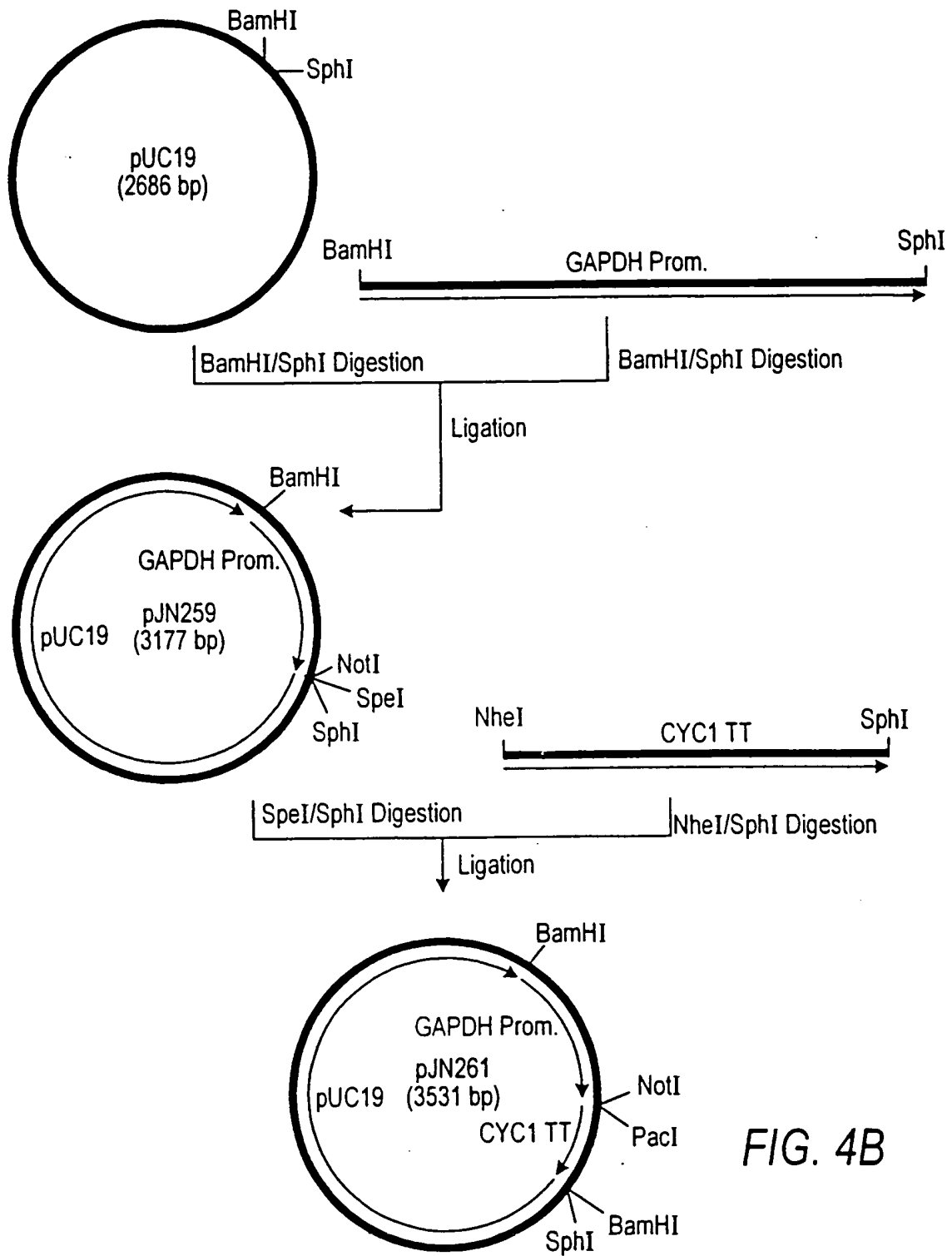


FIG. 4B

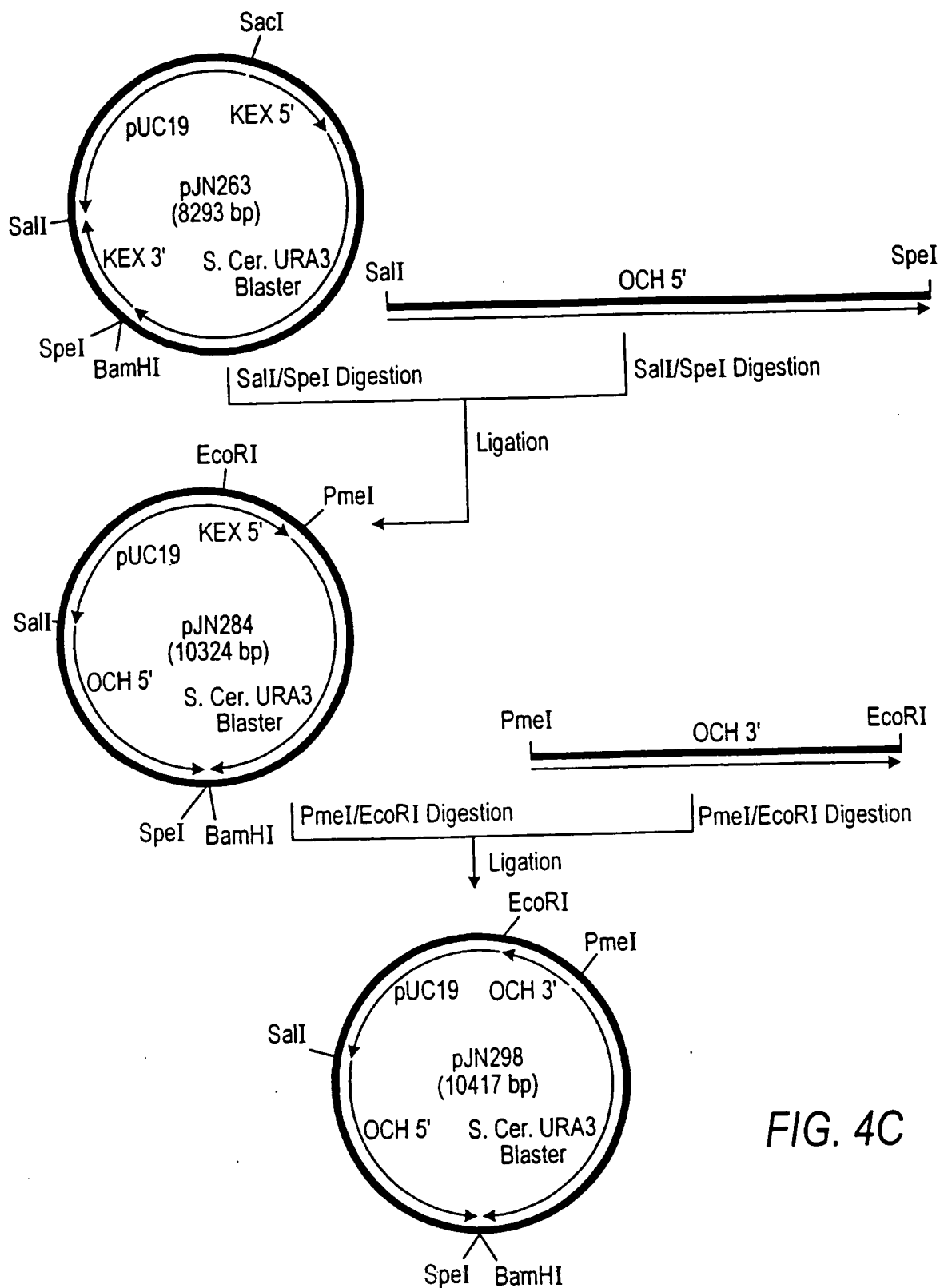


FIG. 4C

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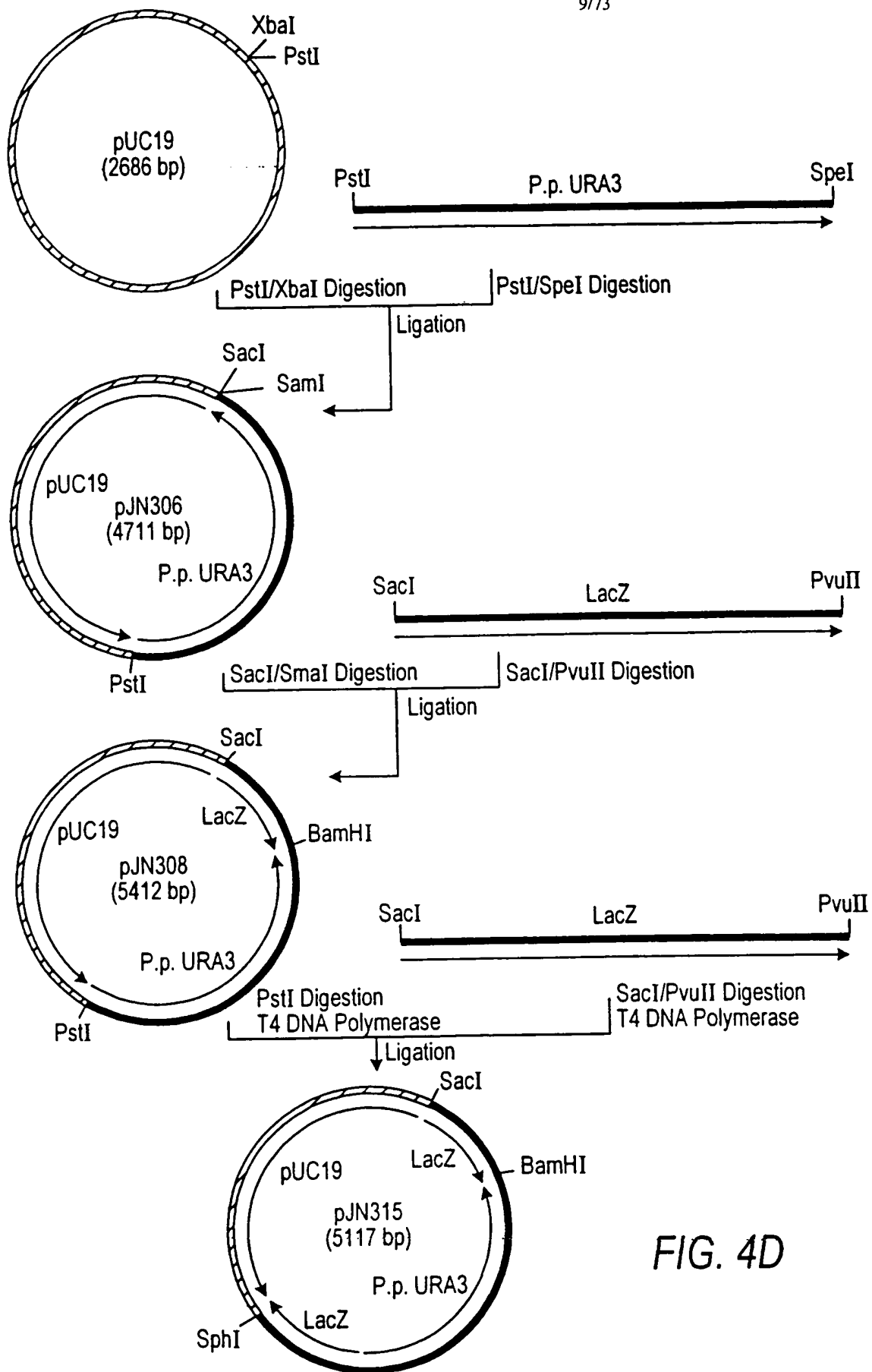


FIG. 4D

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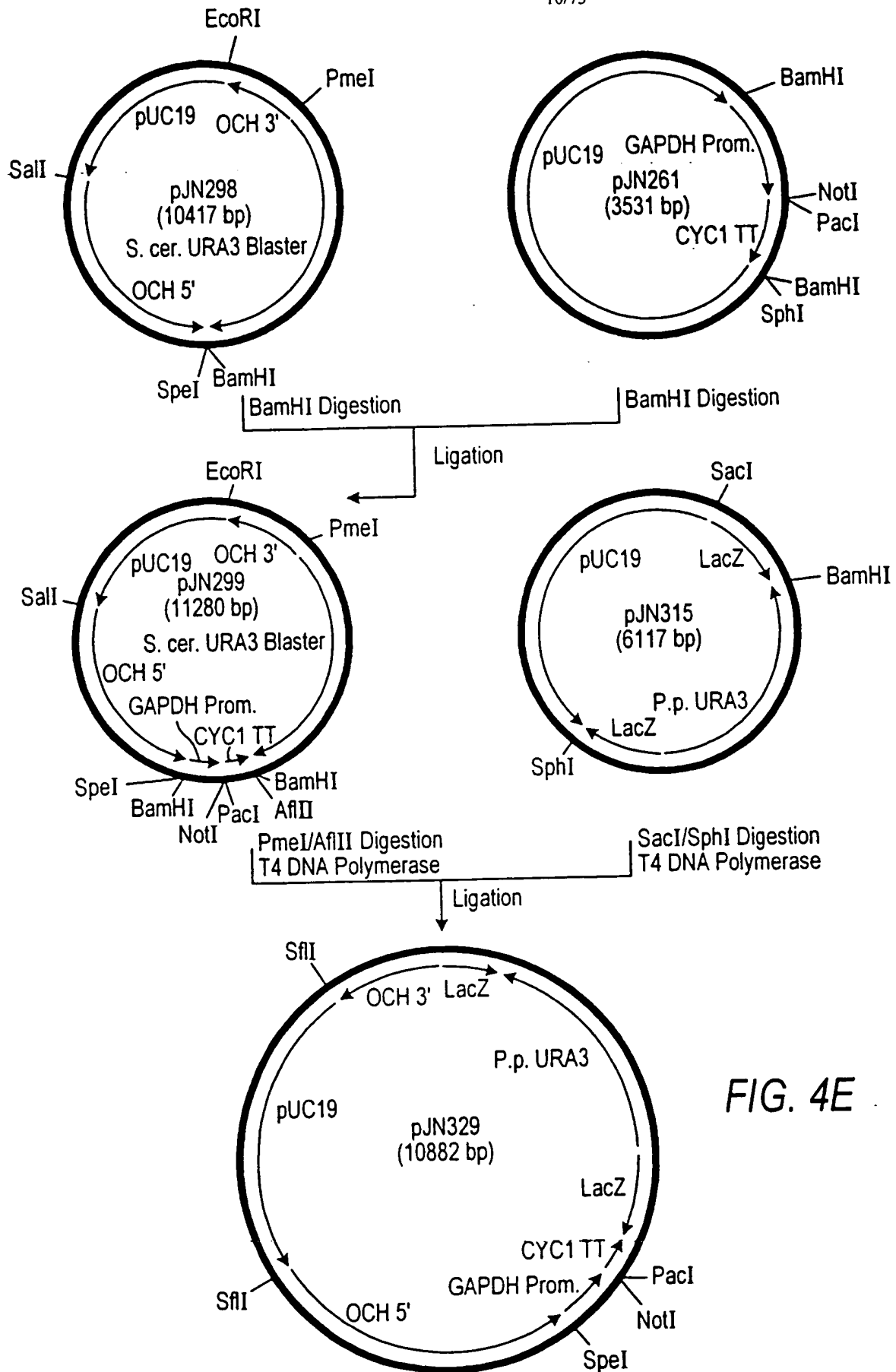


FIG. 4E

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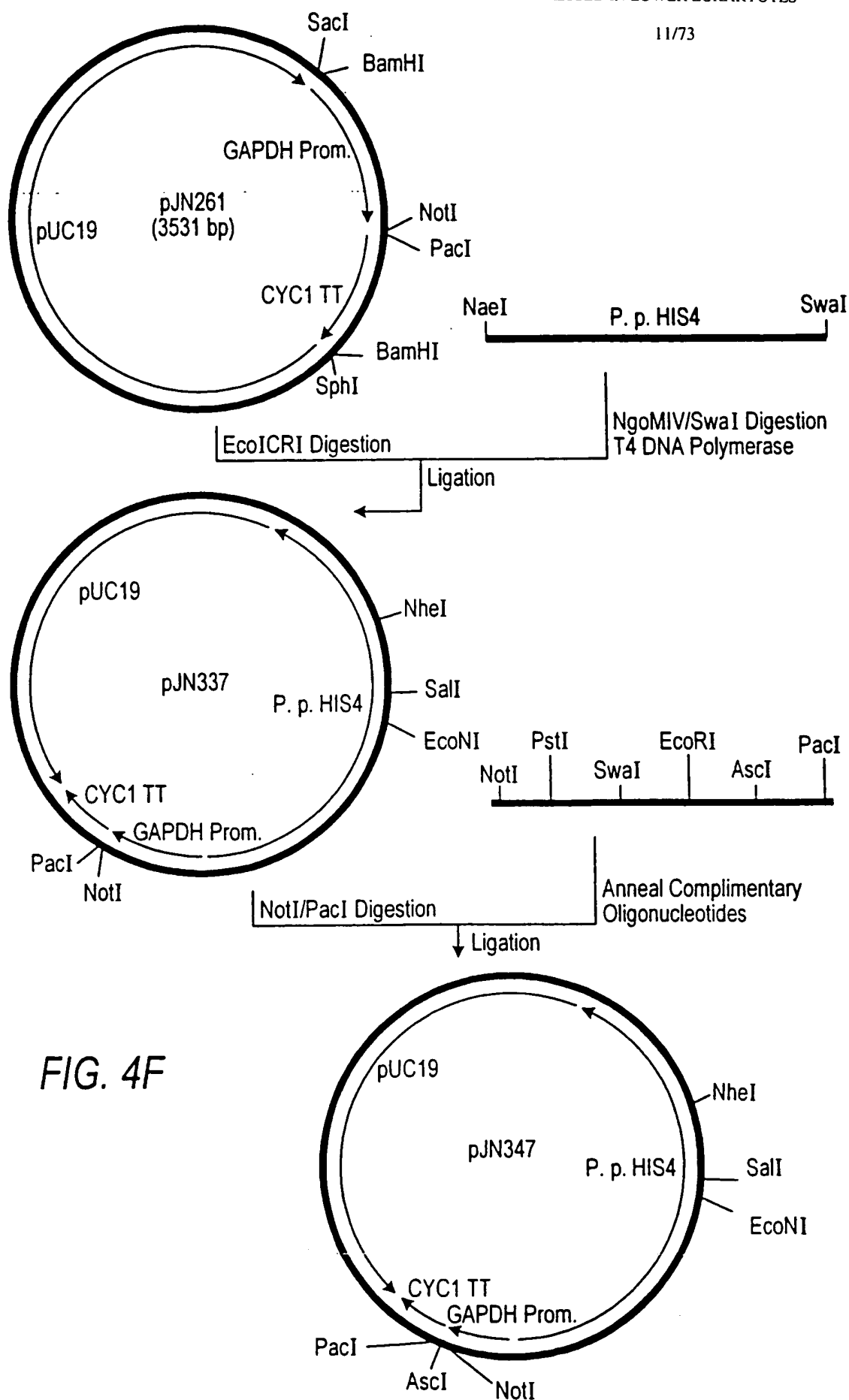


FIG. 4F

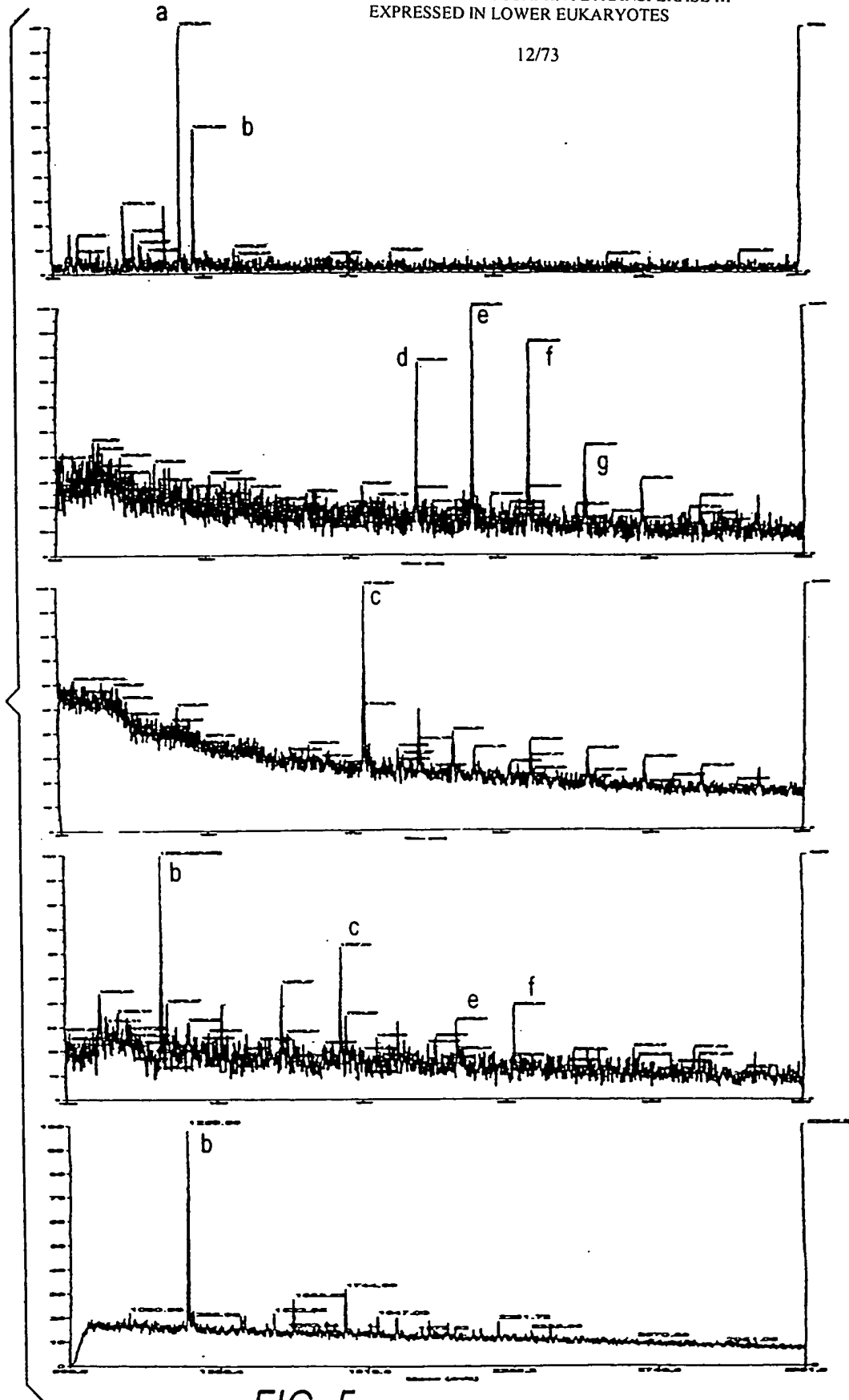
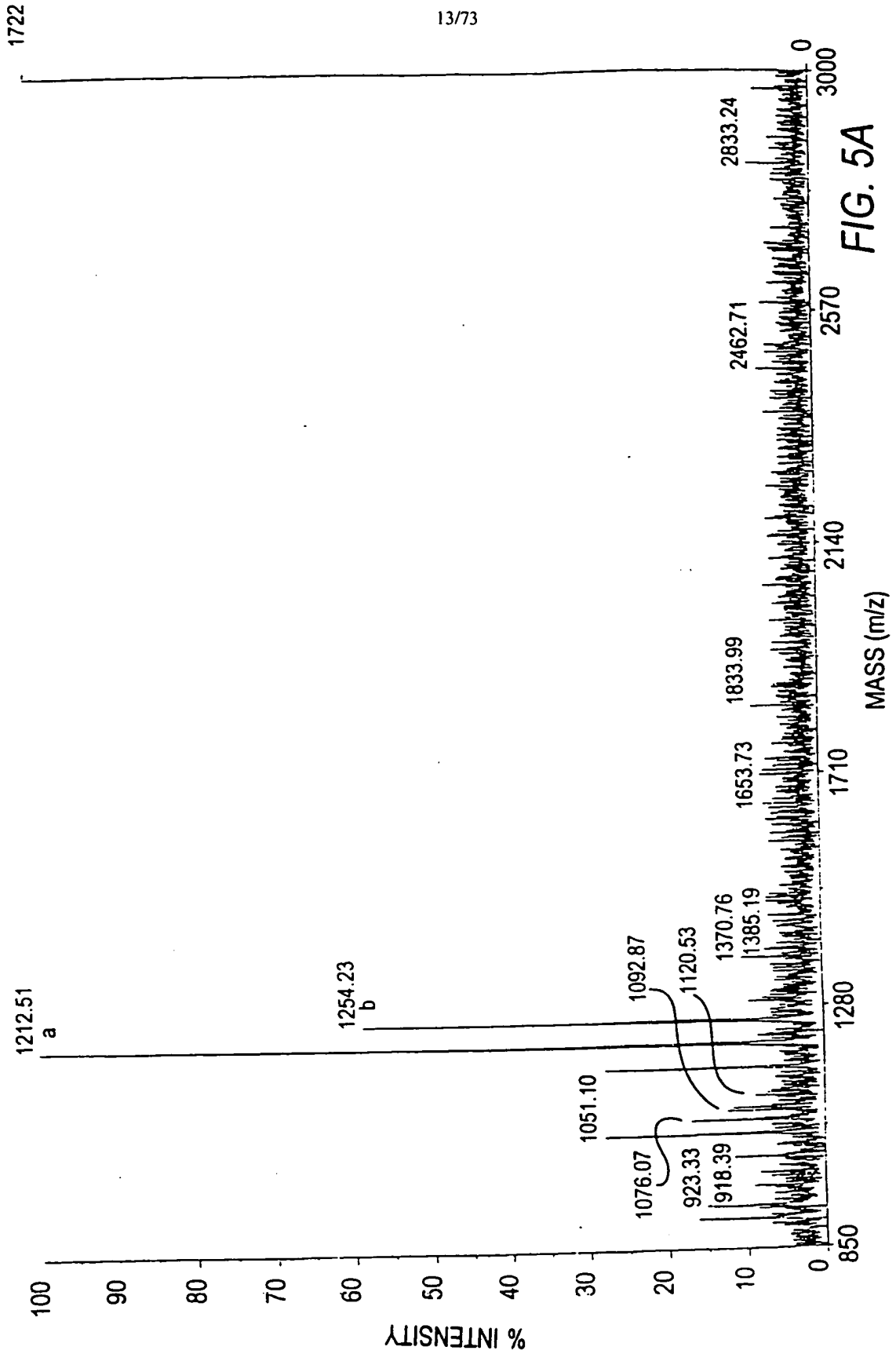


FIG. 5

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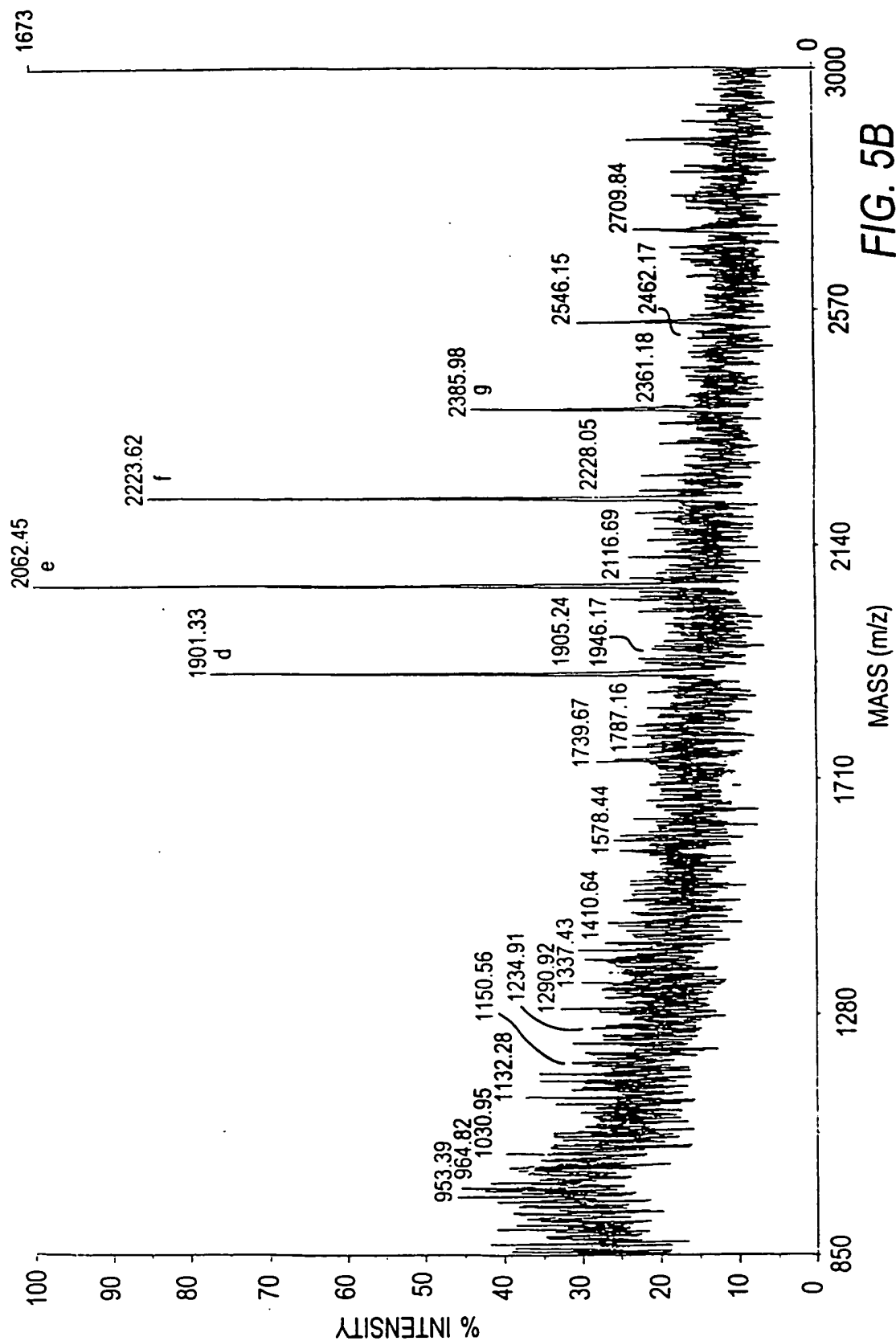


FIG. 5B

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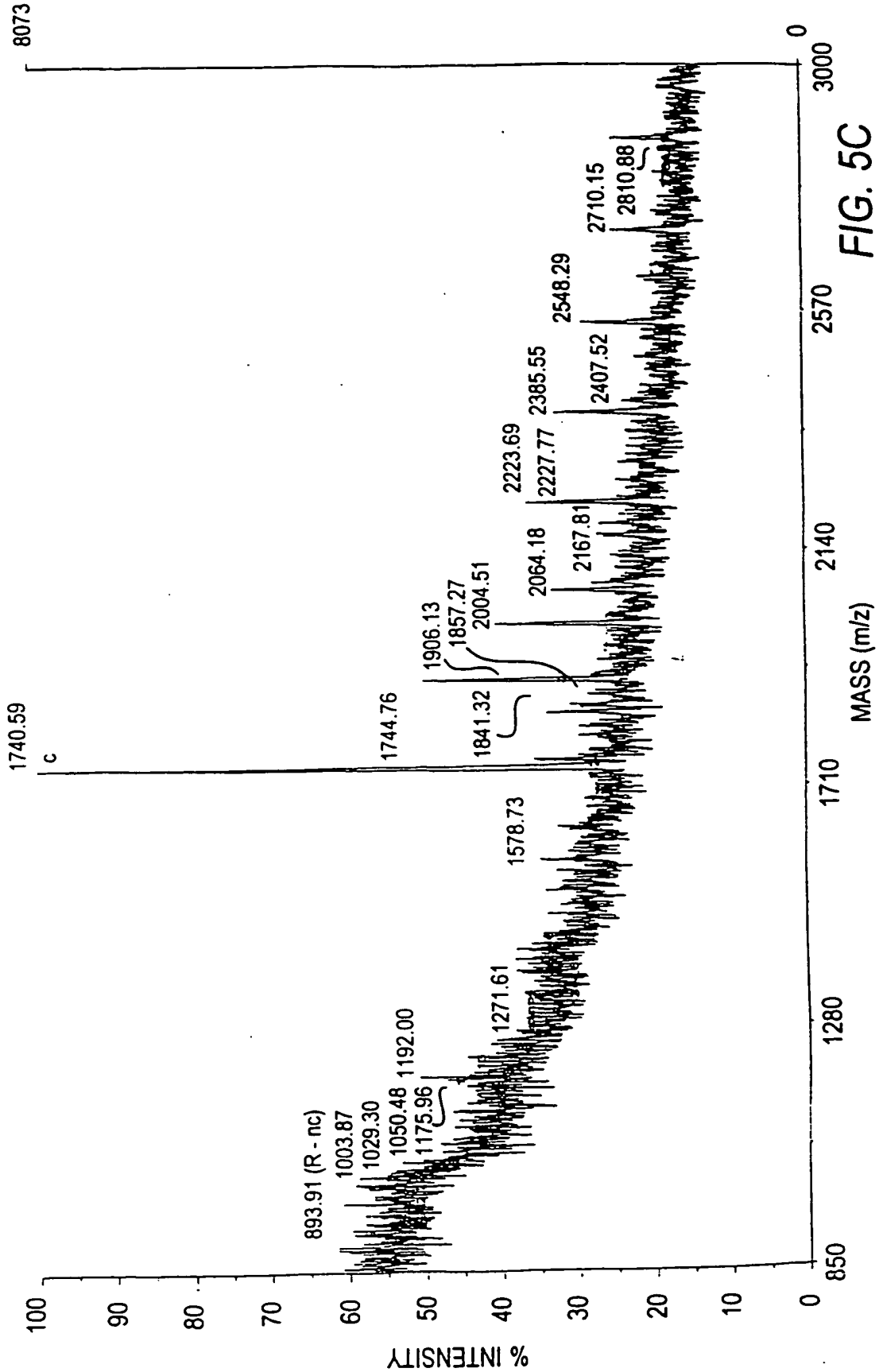


FIG. 5C

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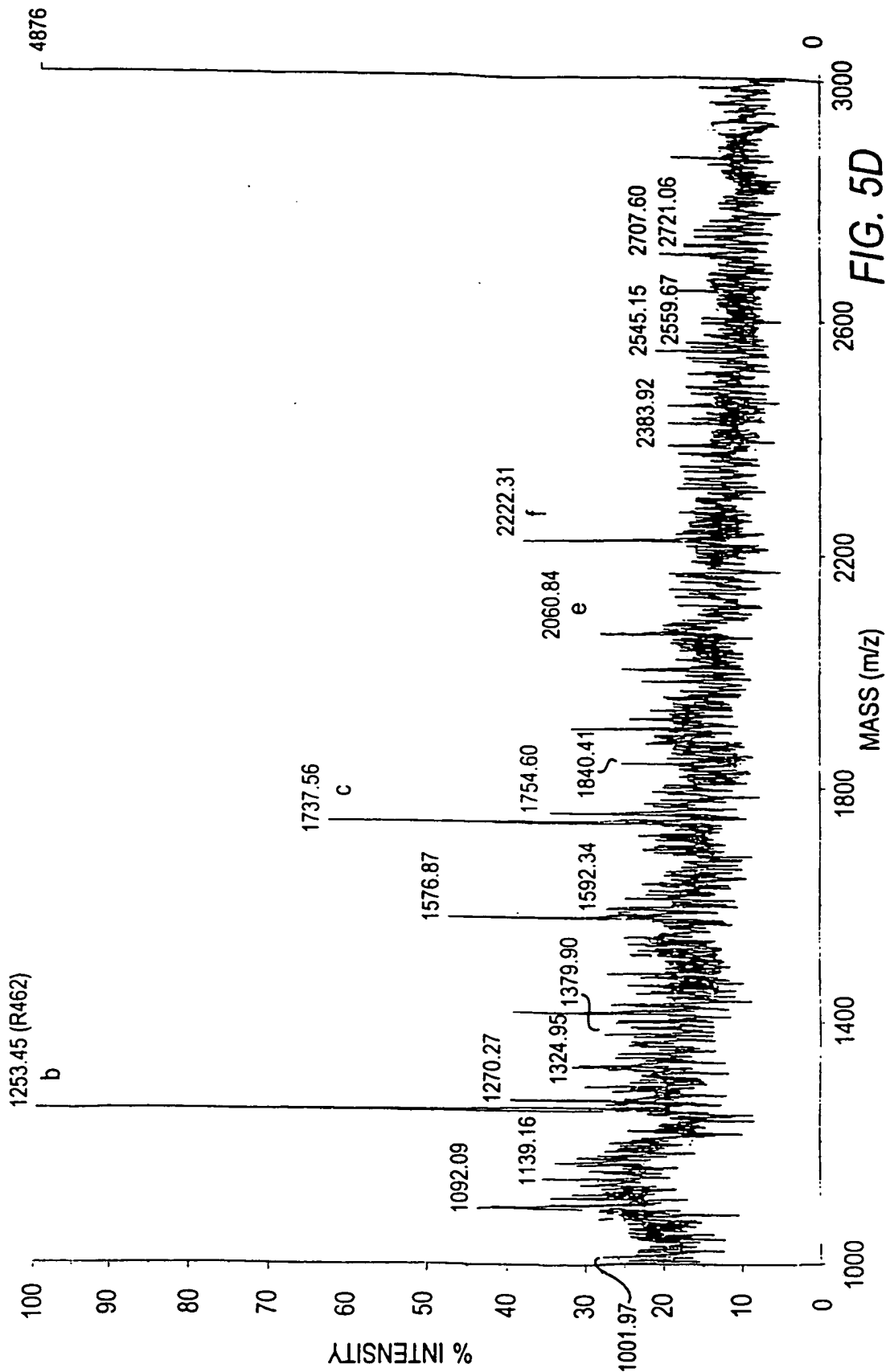
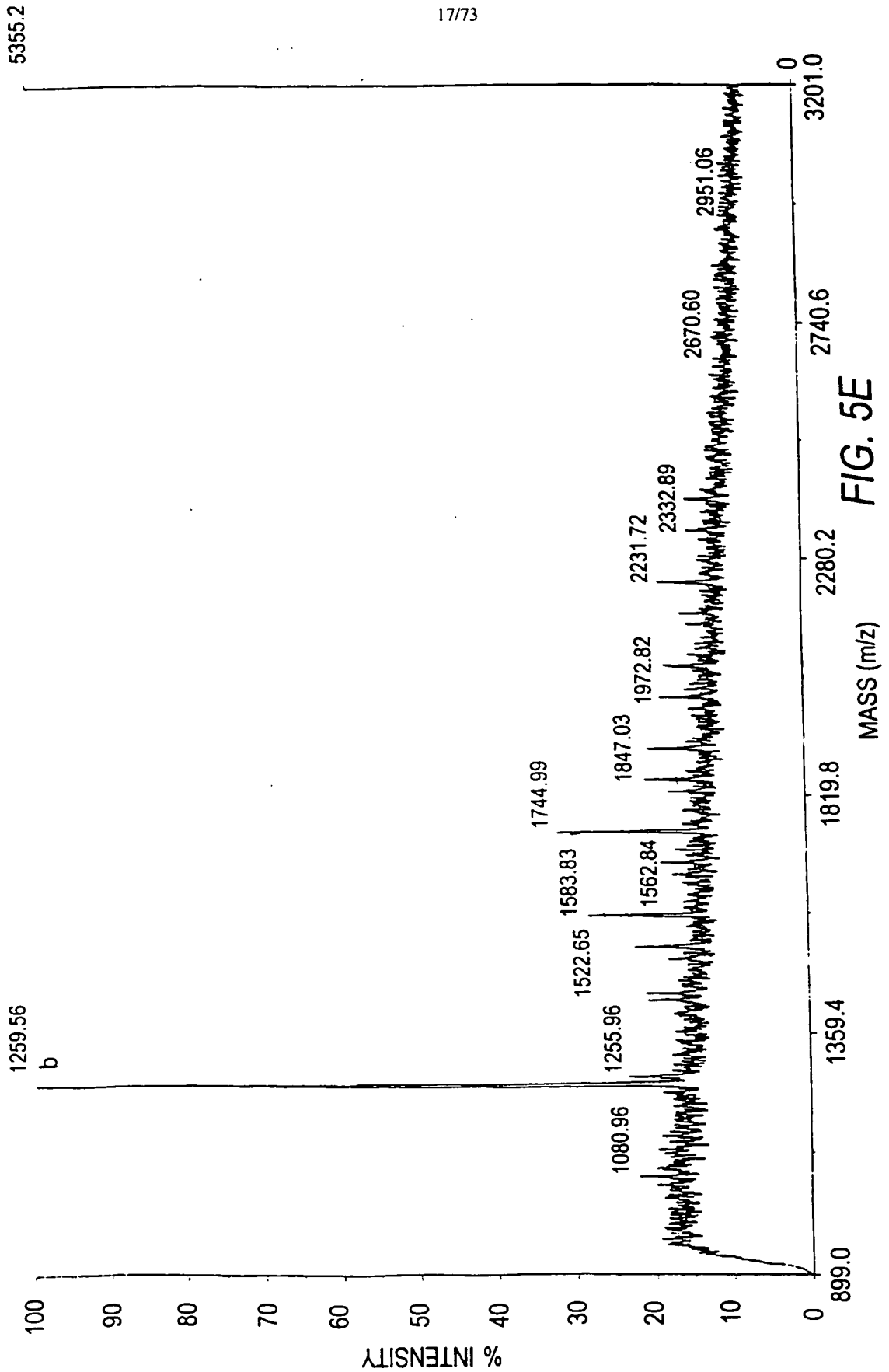


FIG. 5D

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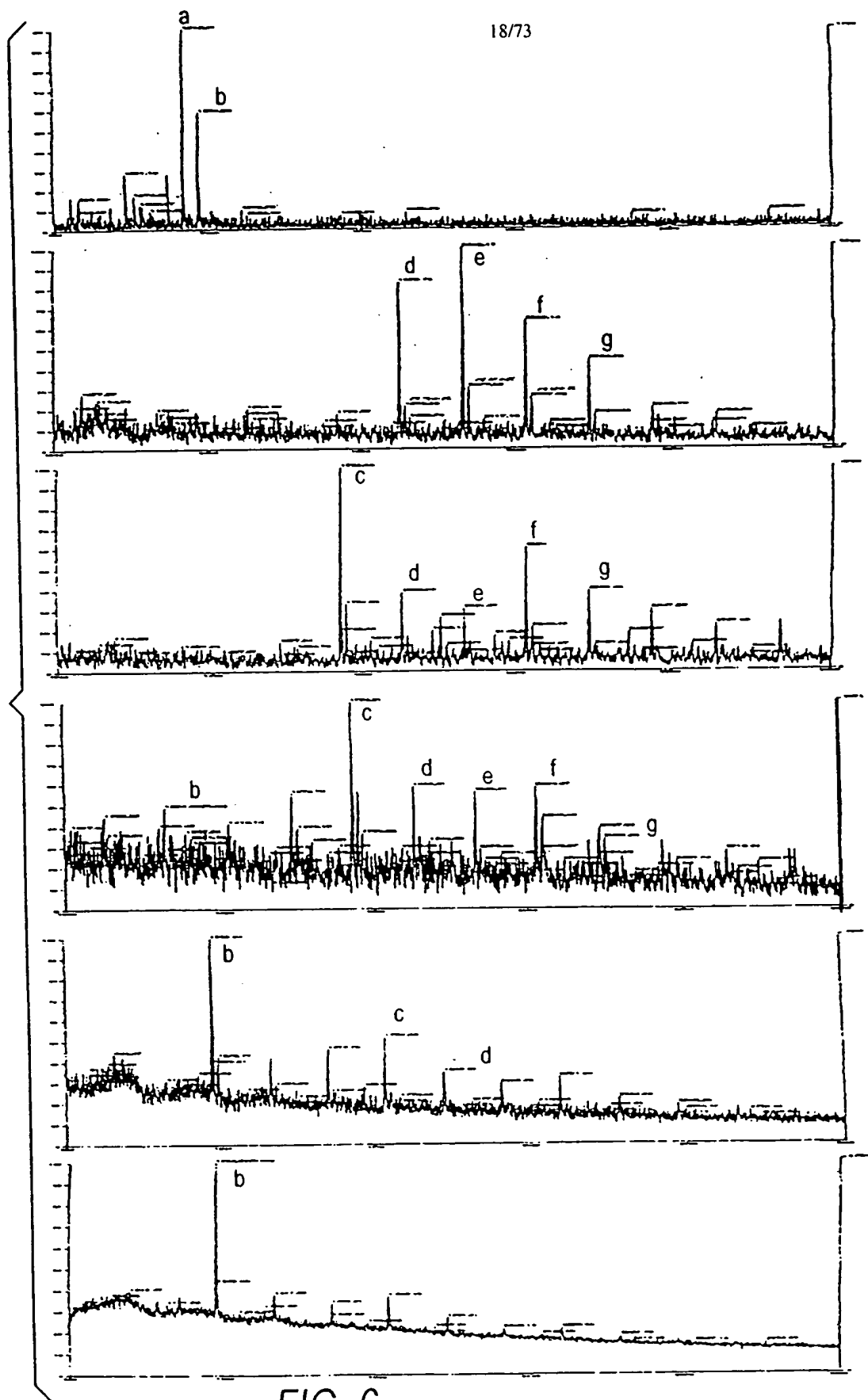
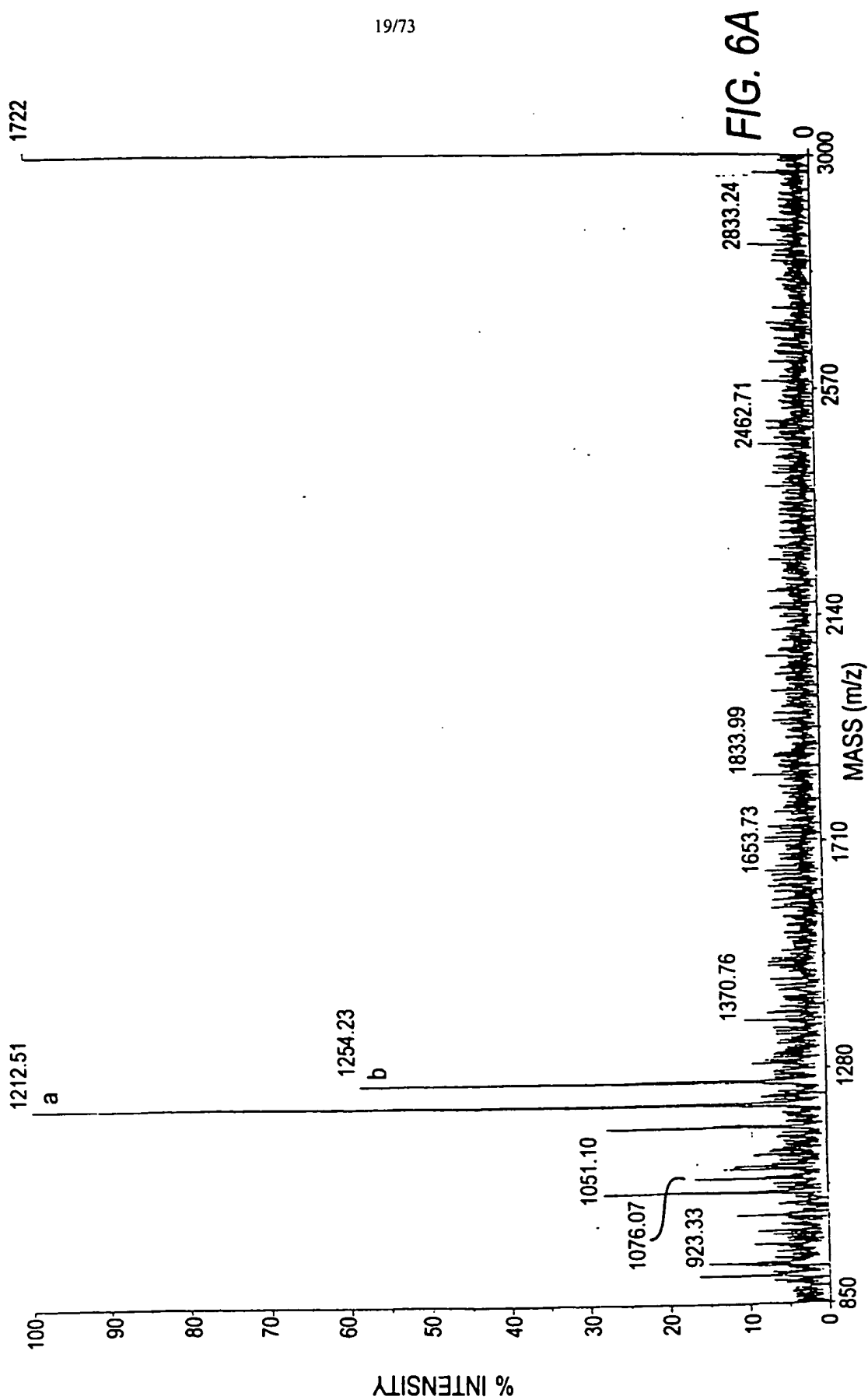
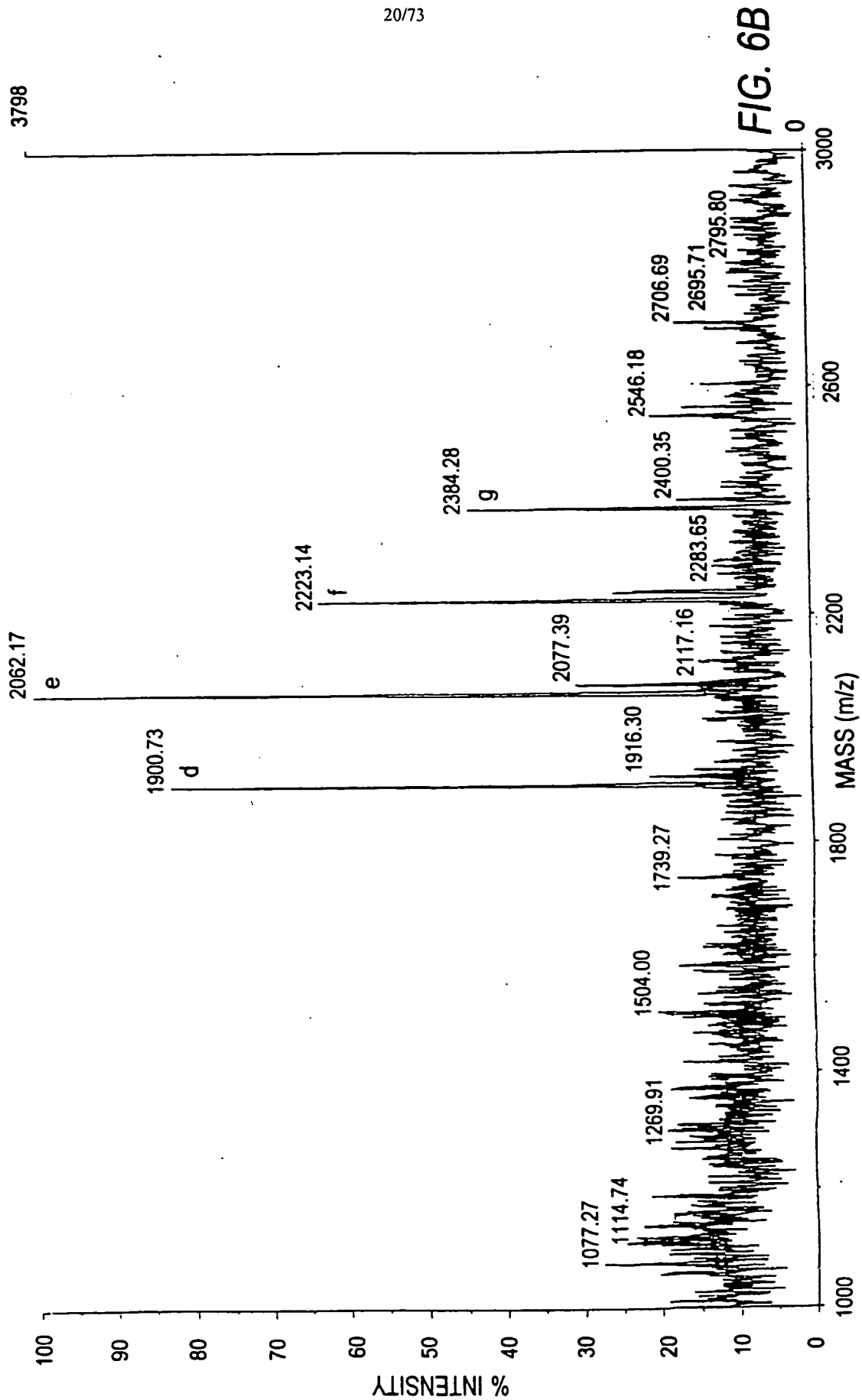


FIG. 6

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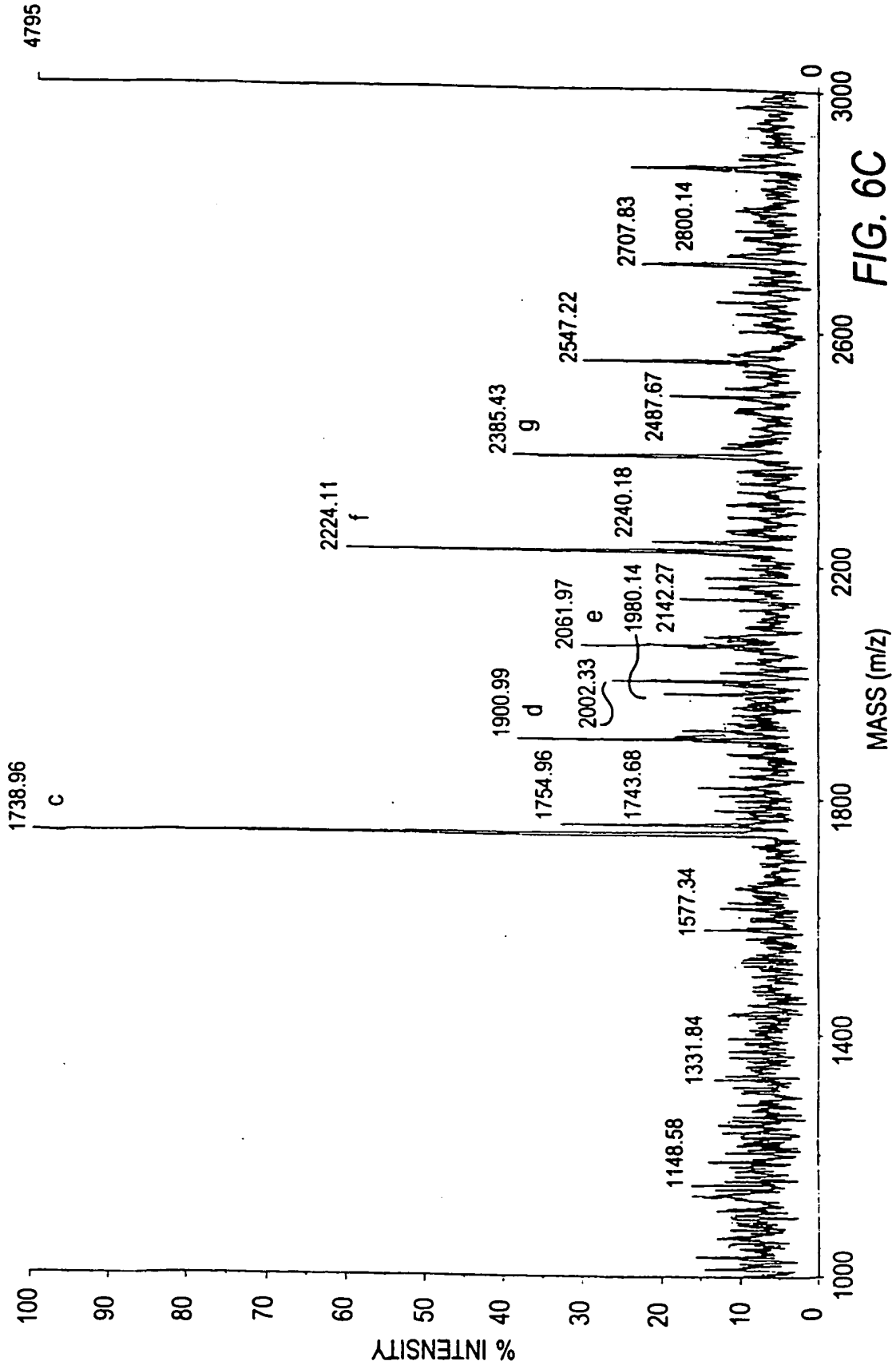
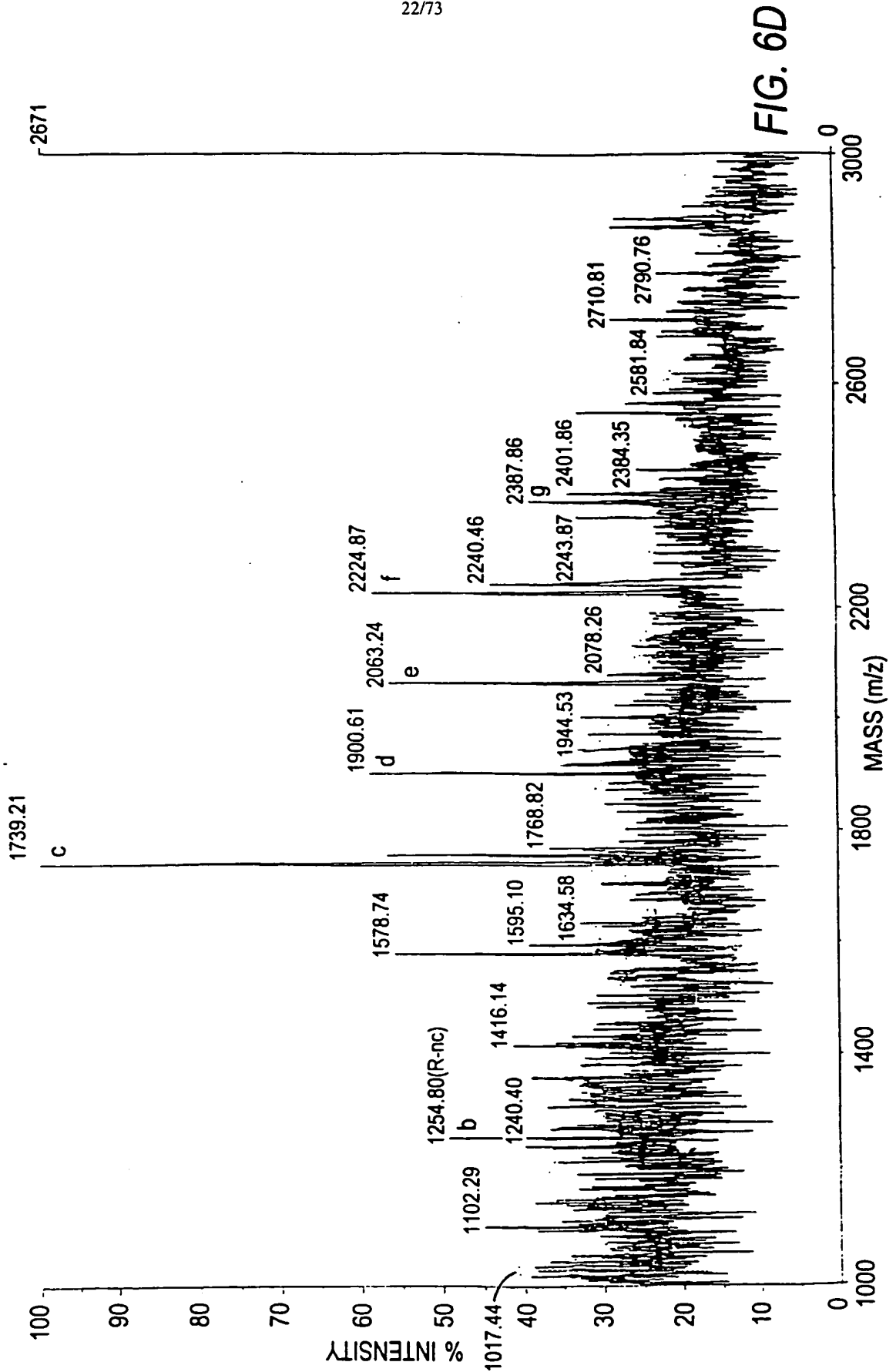


FIG. 6C

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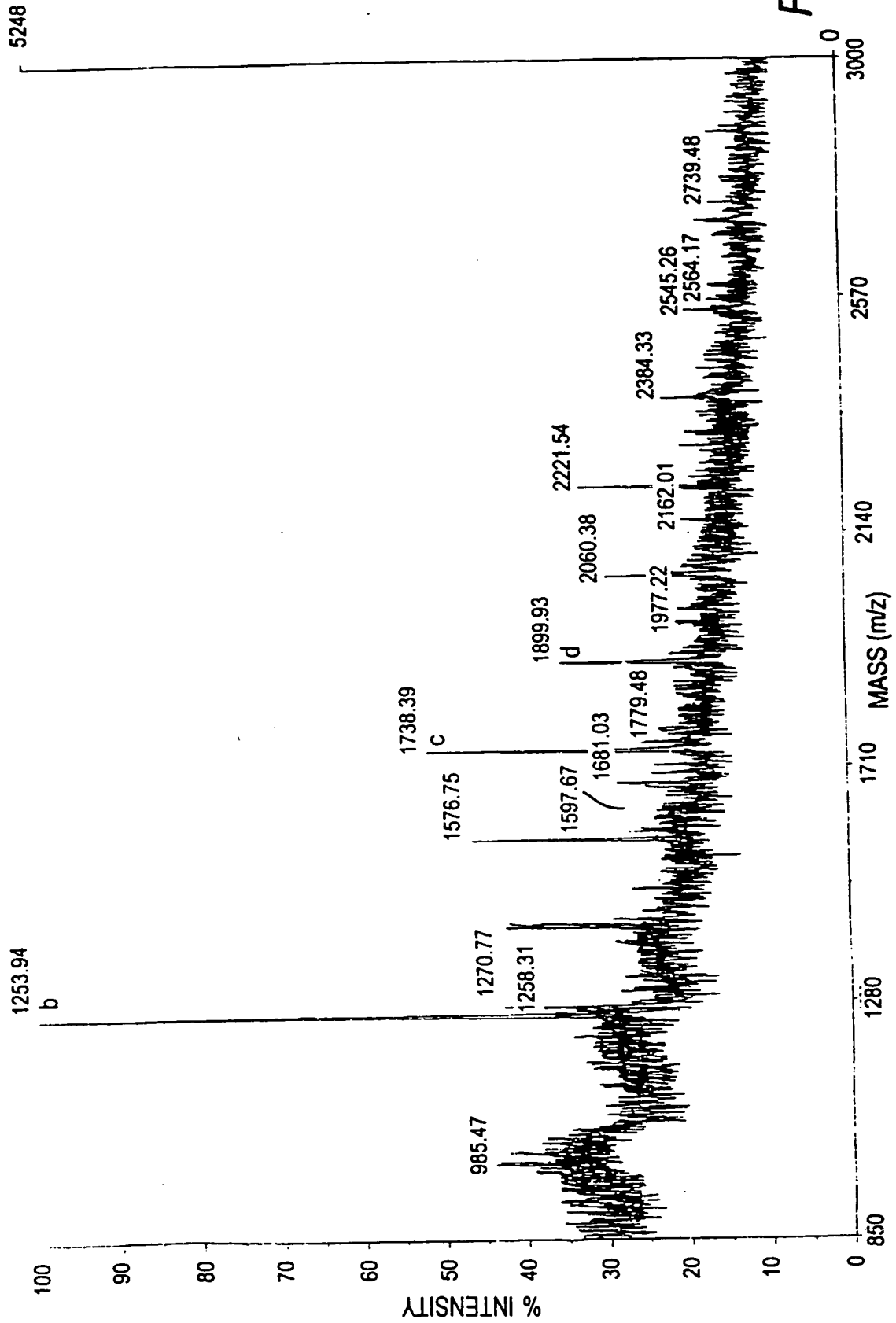
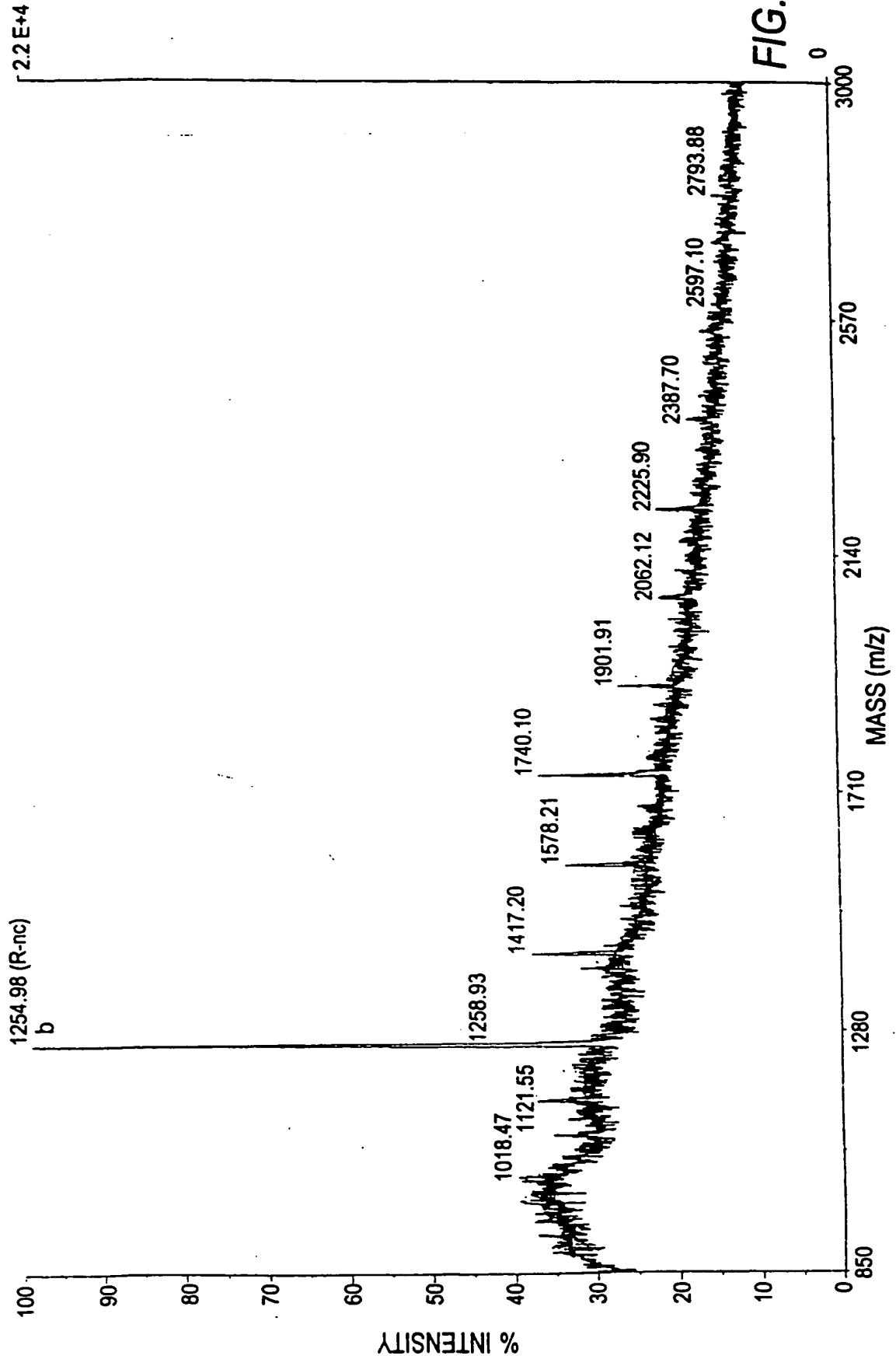


FIG. 6E

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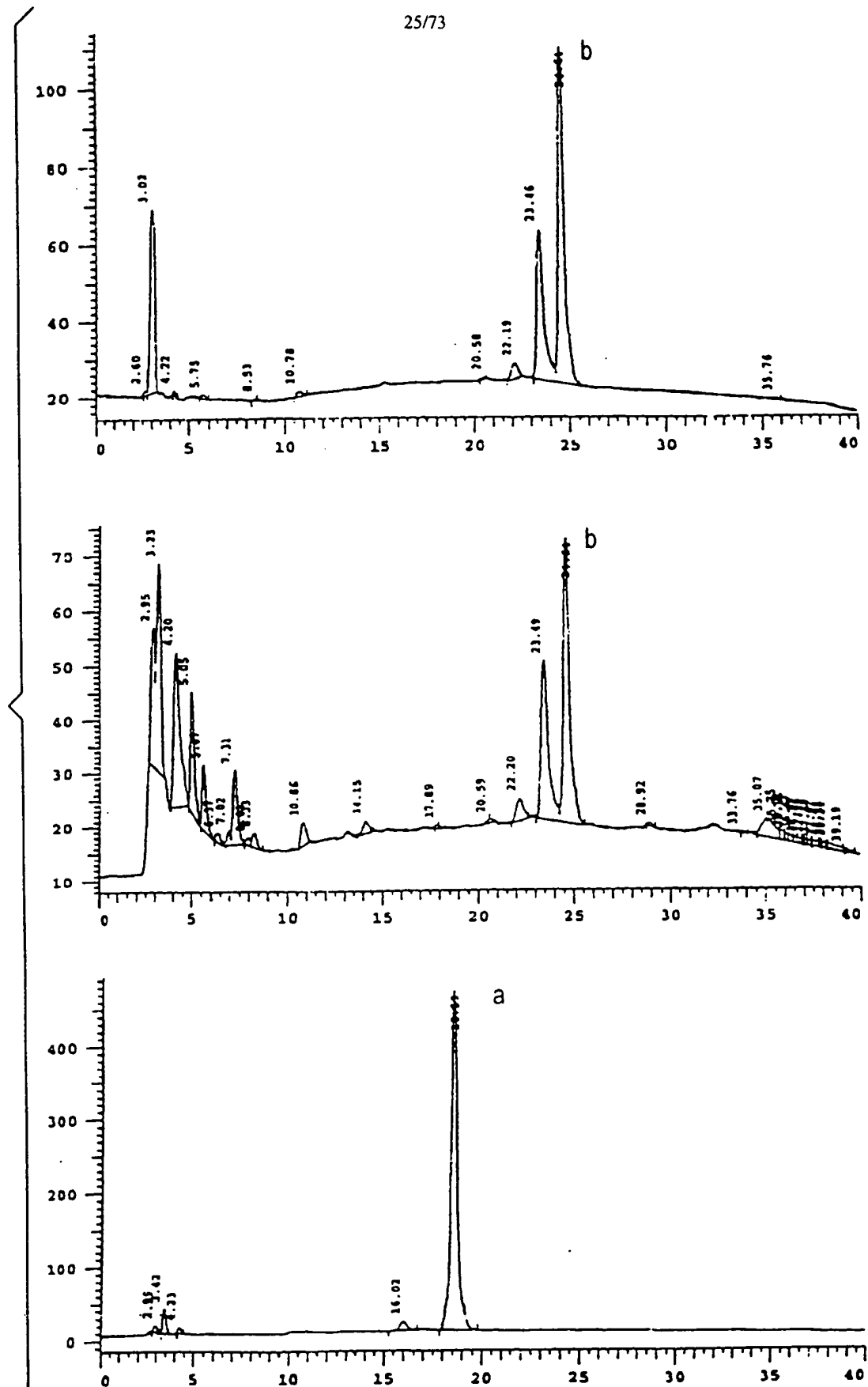


FIG. 7

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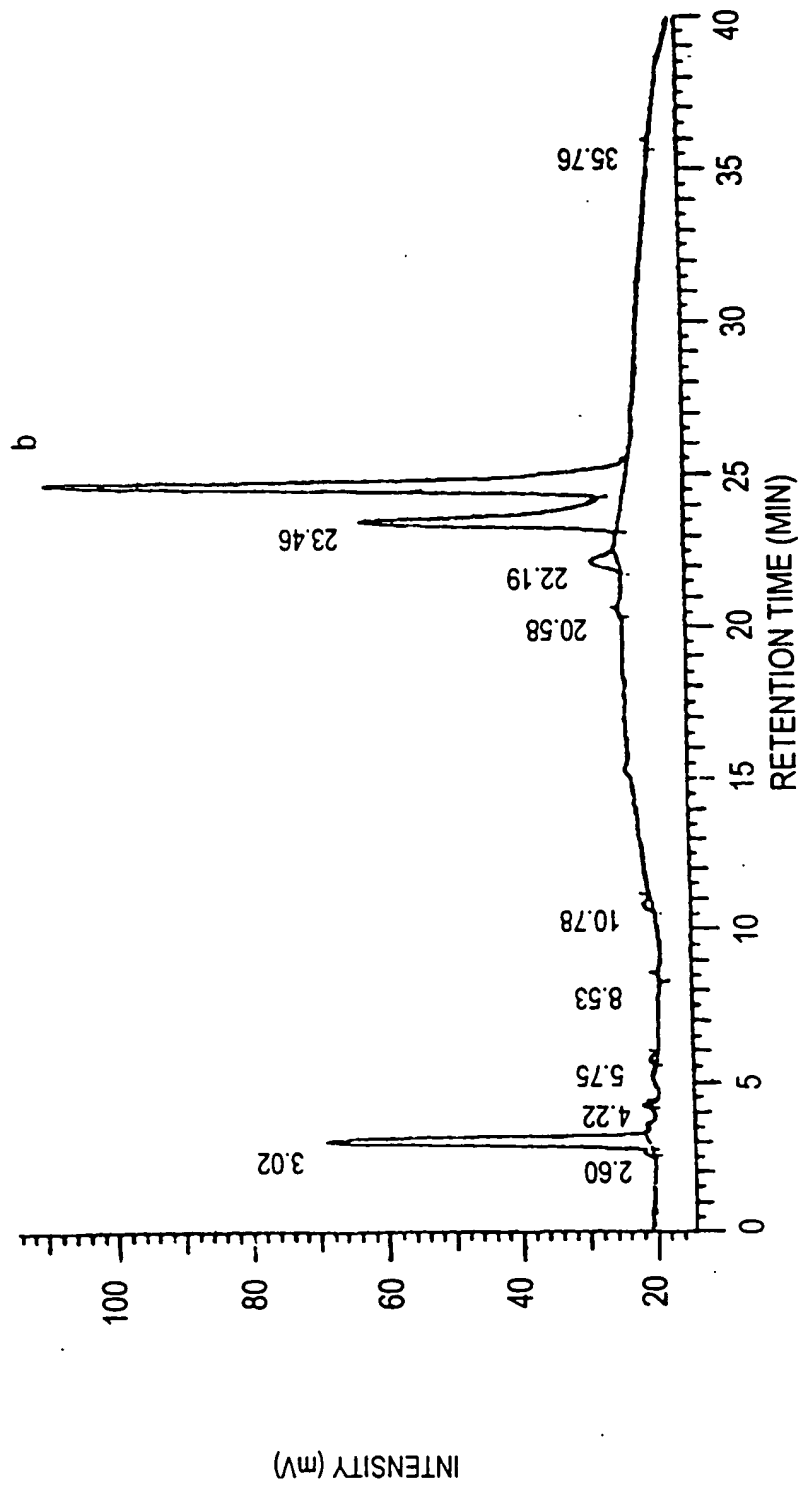


FIG. 7A

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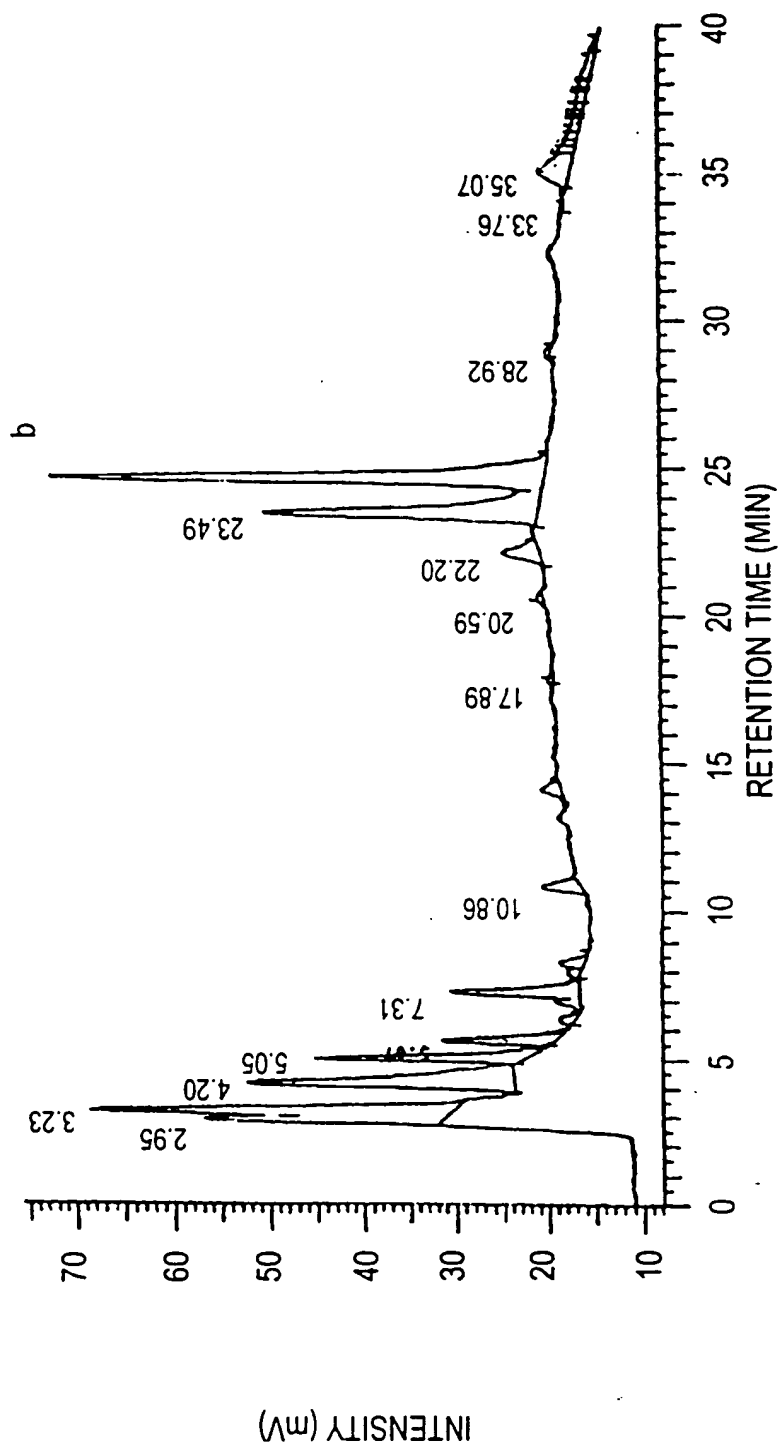


FIG. 7B

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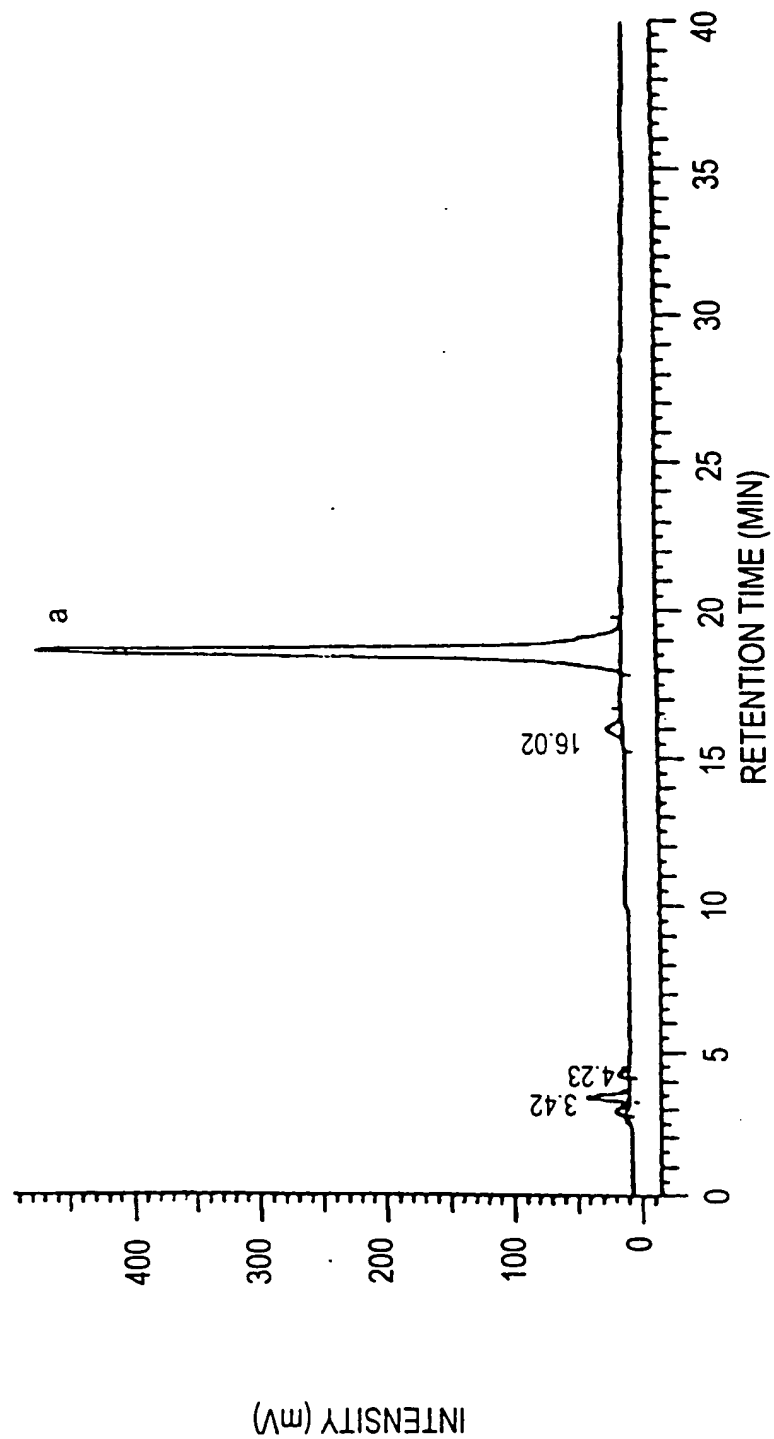


FIG. 7C

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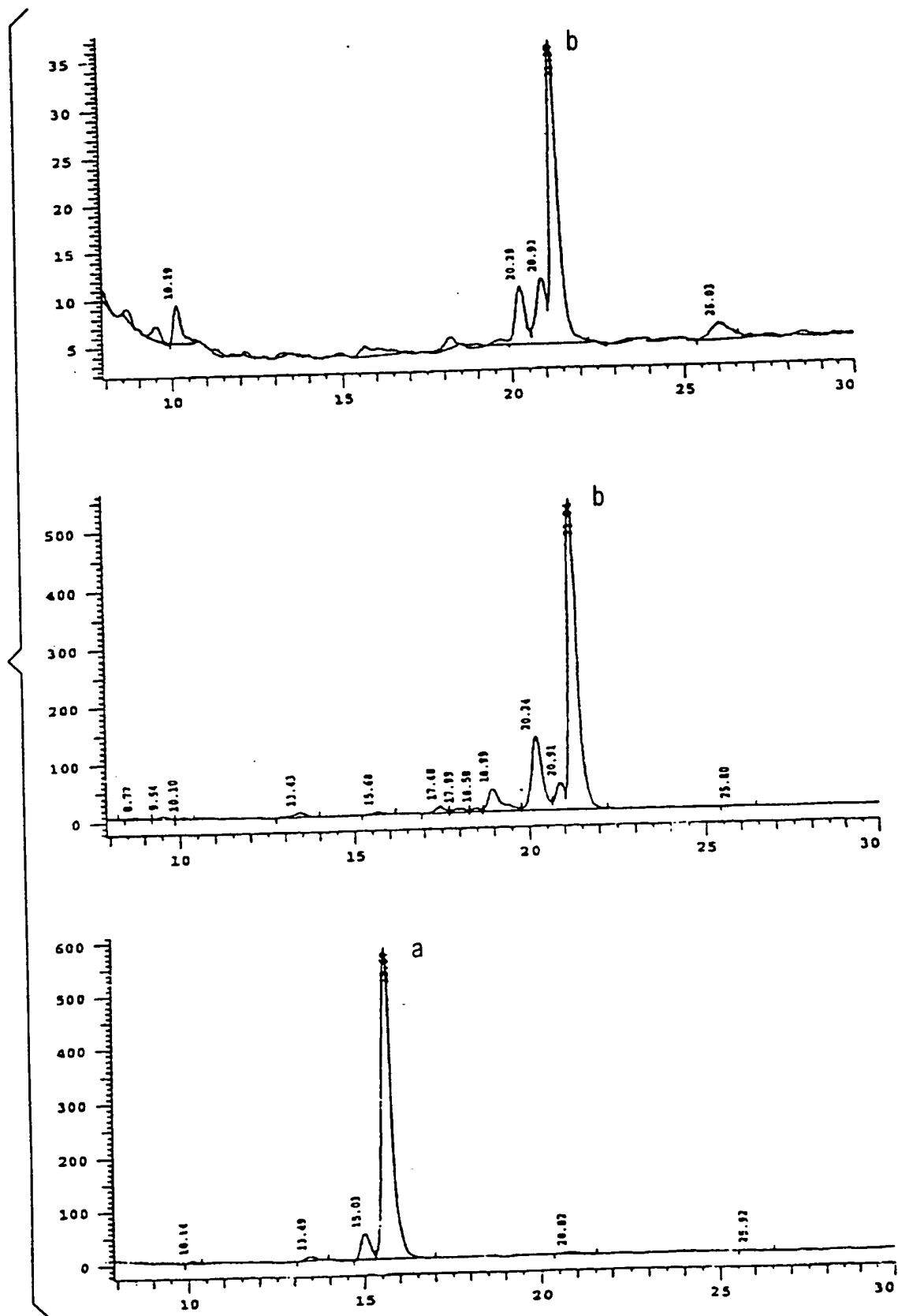


FIG. 8

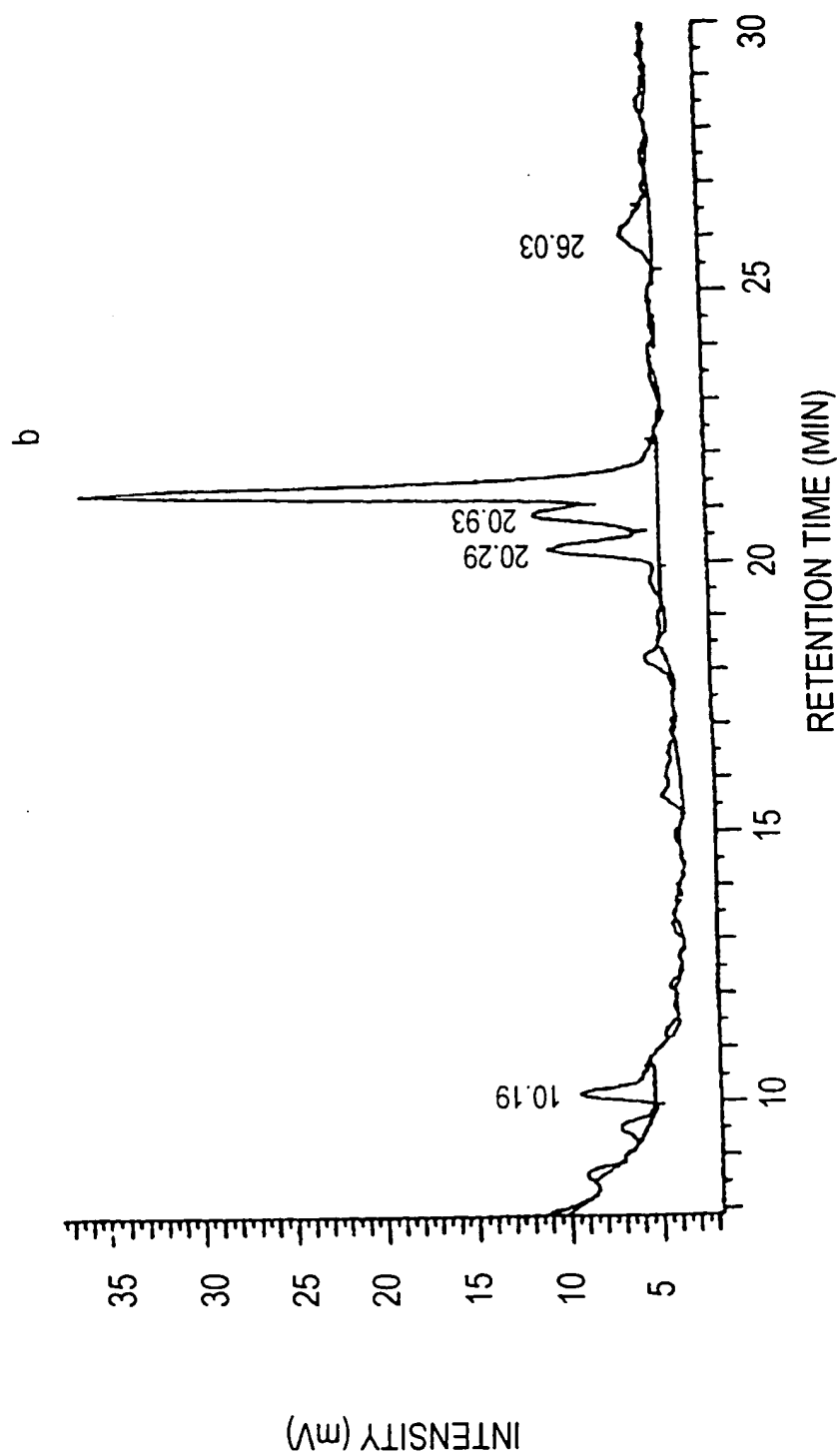


FIG. 8A

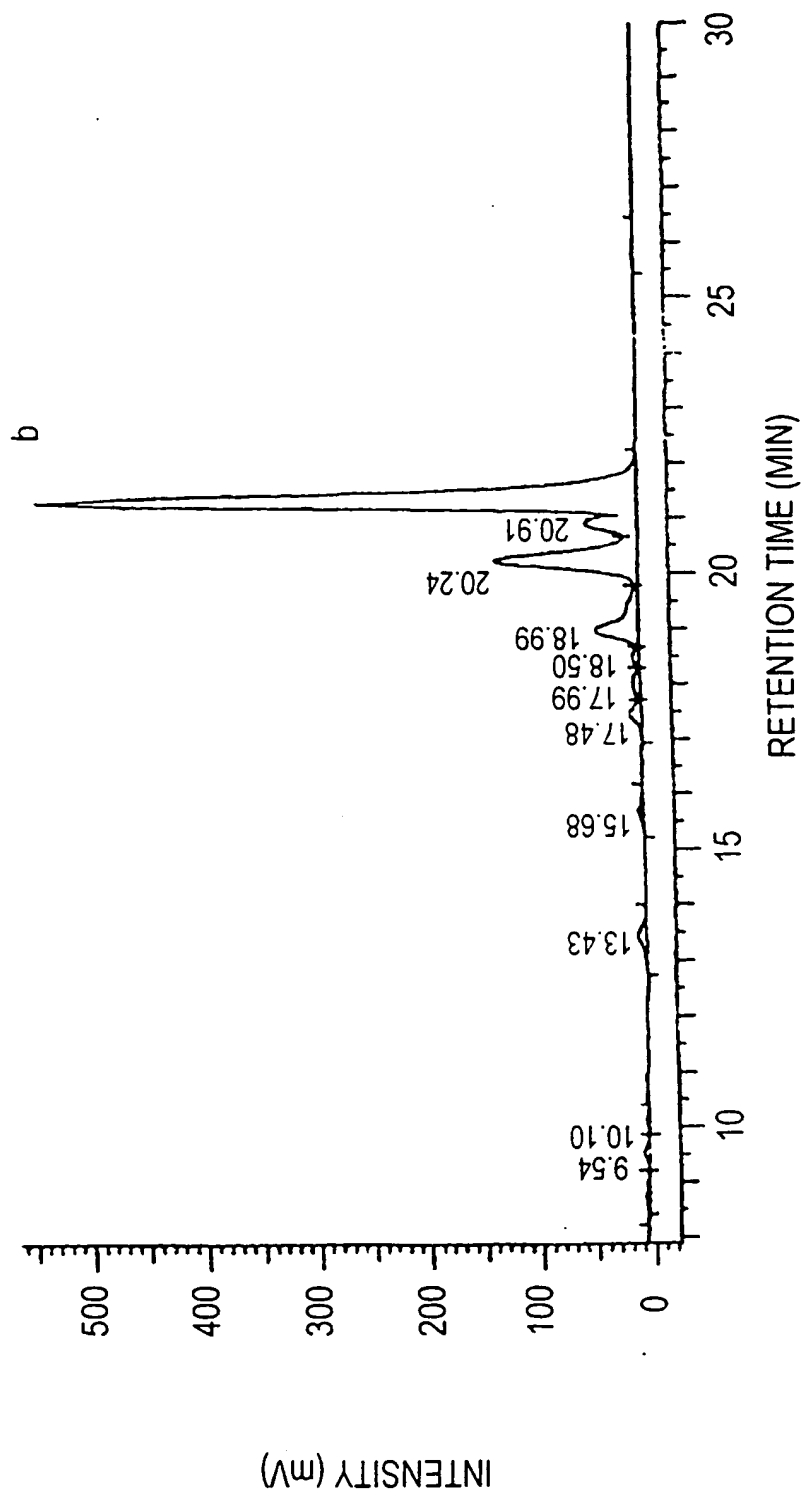


FIG. 8B

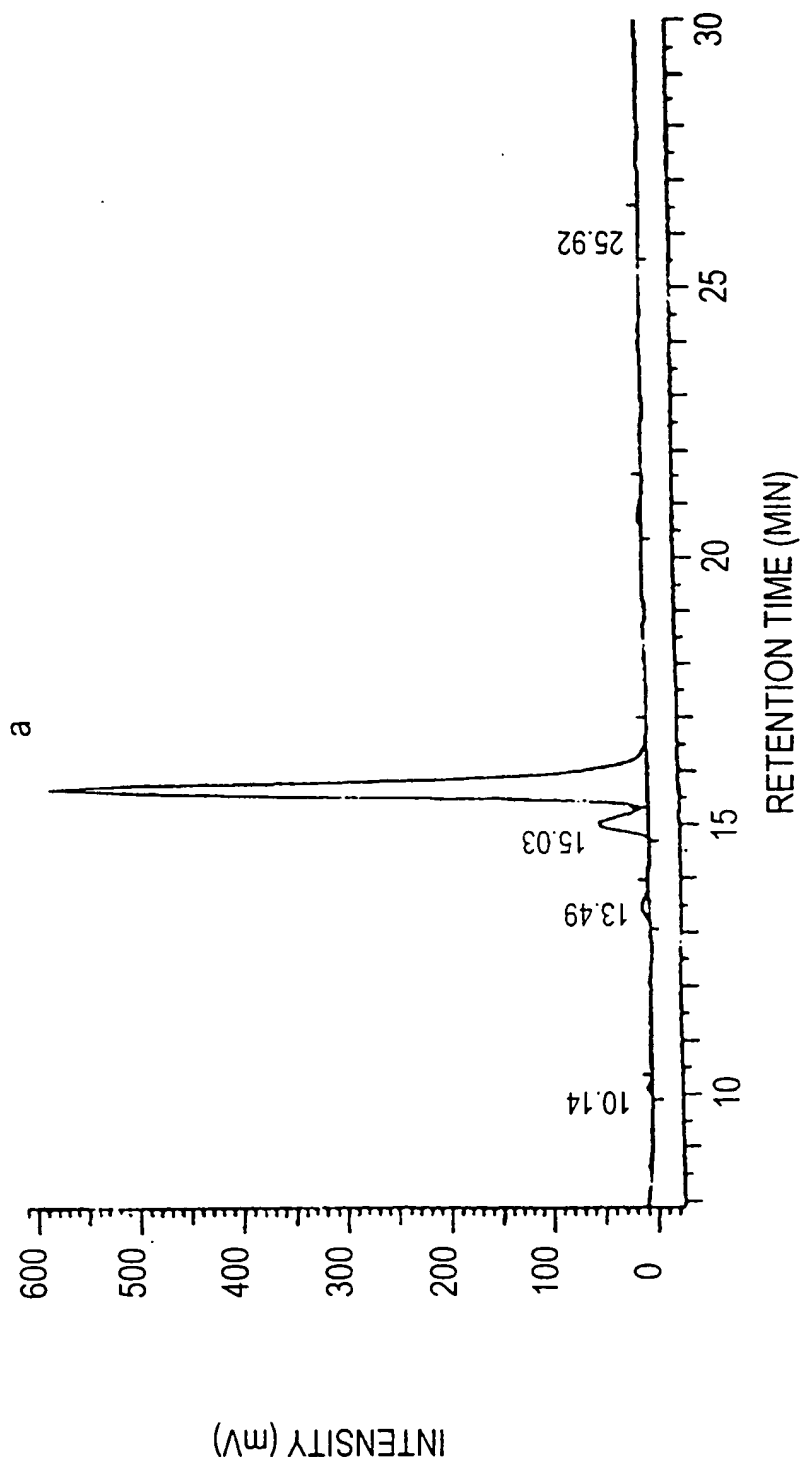
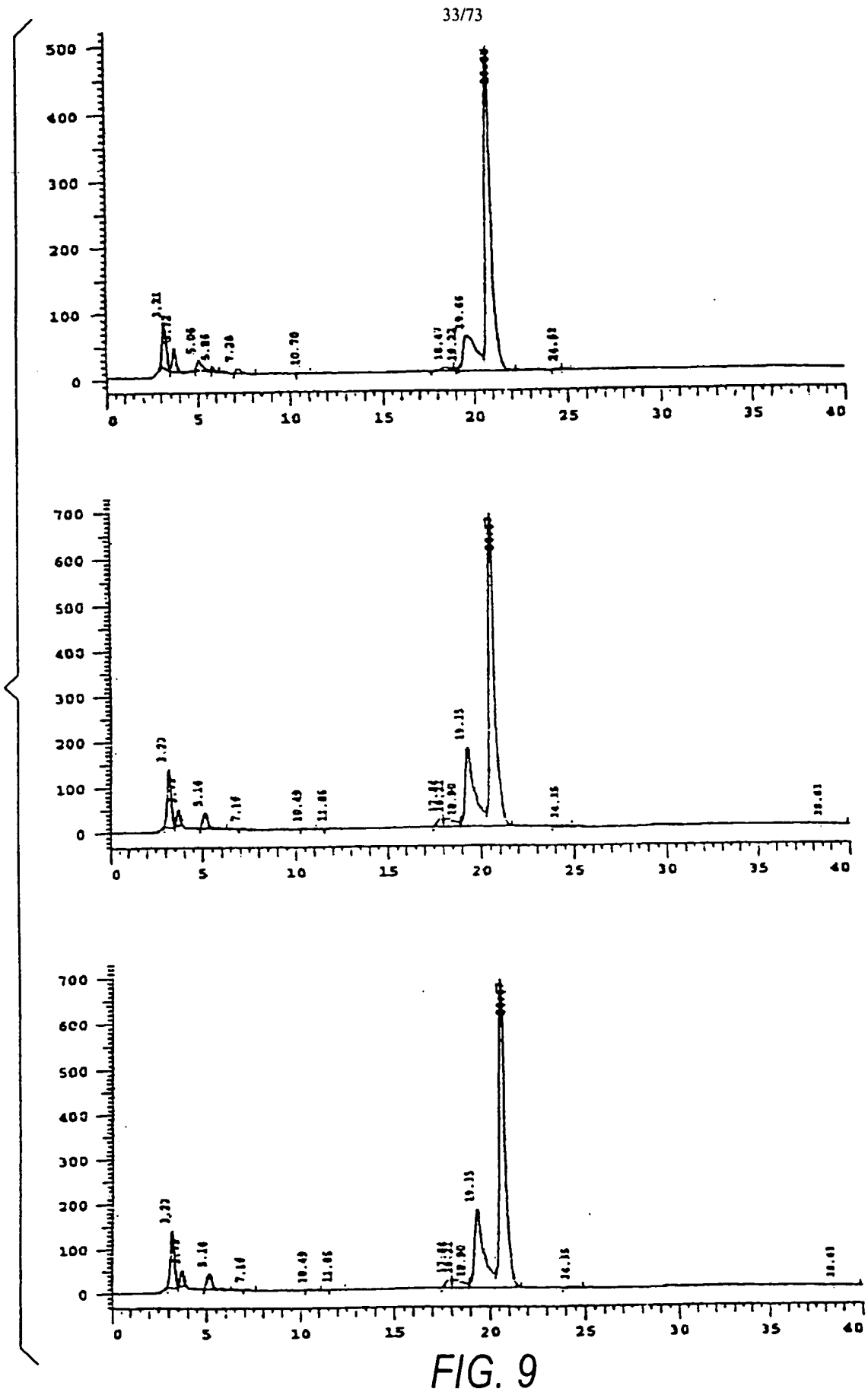


FIG. 8C



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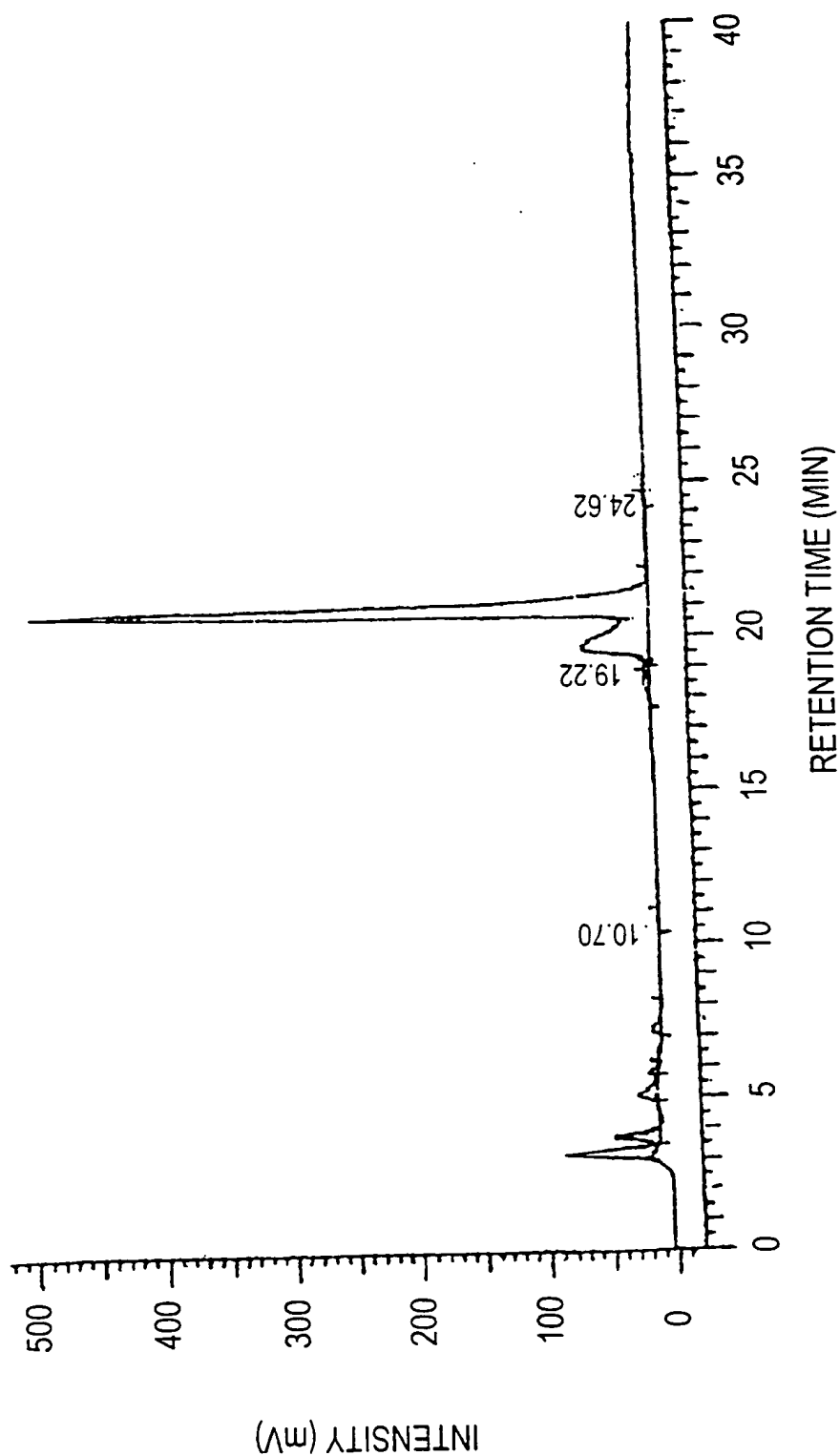


FIG. 9A

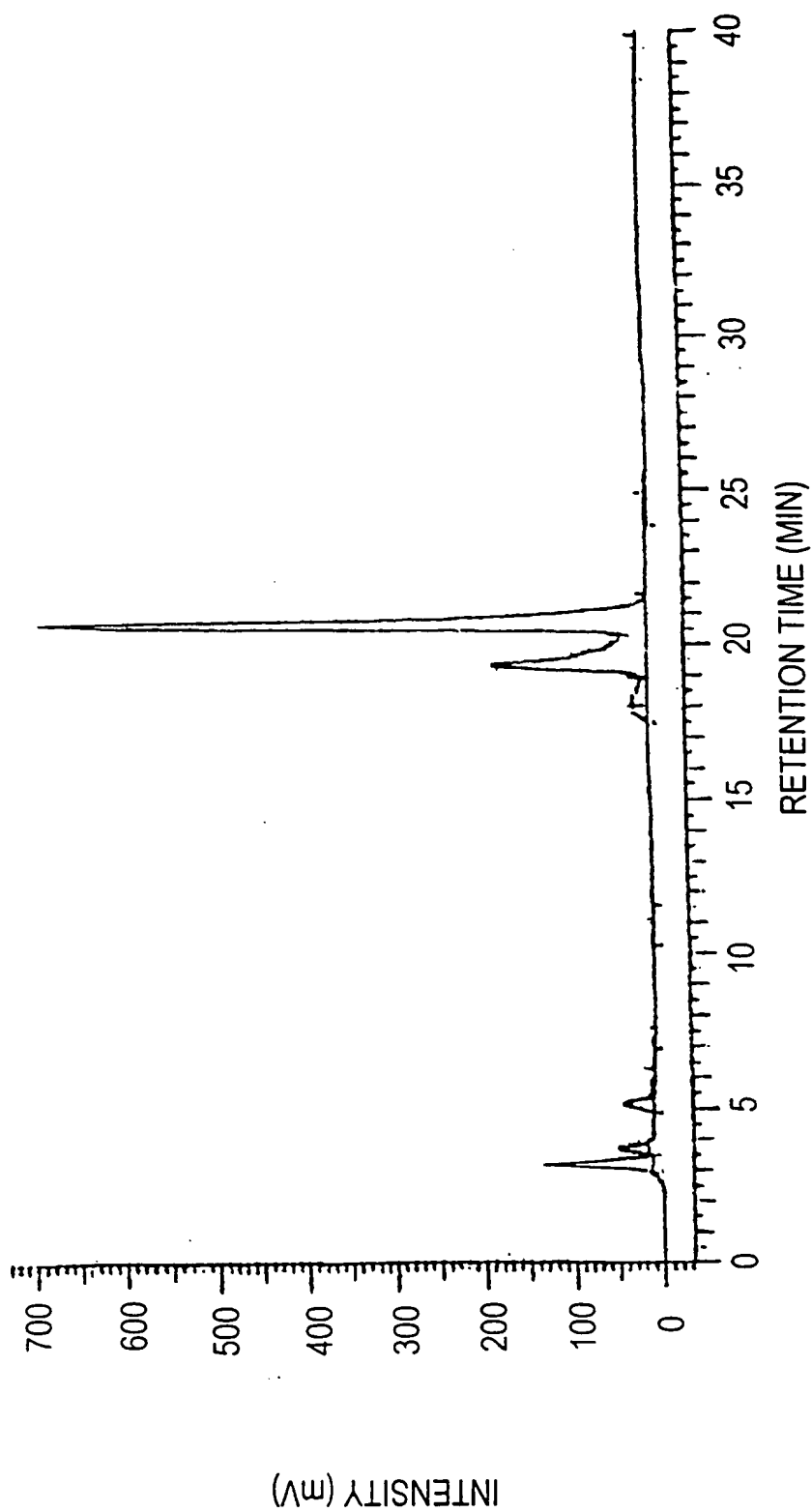


FIG. 9B

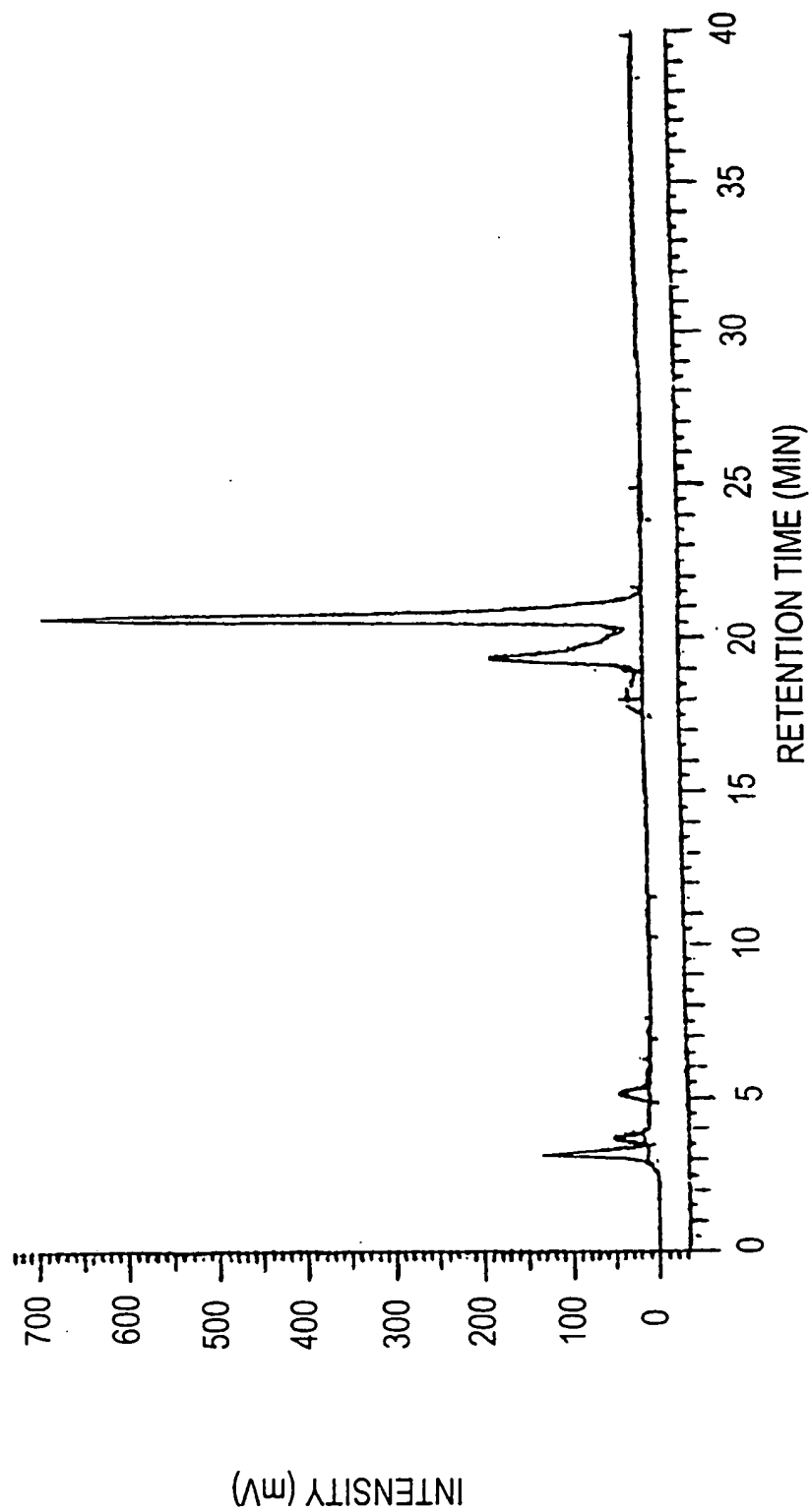
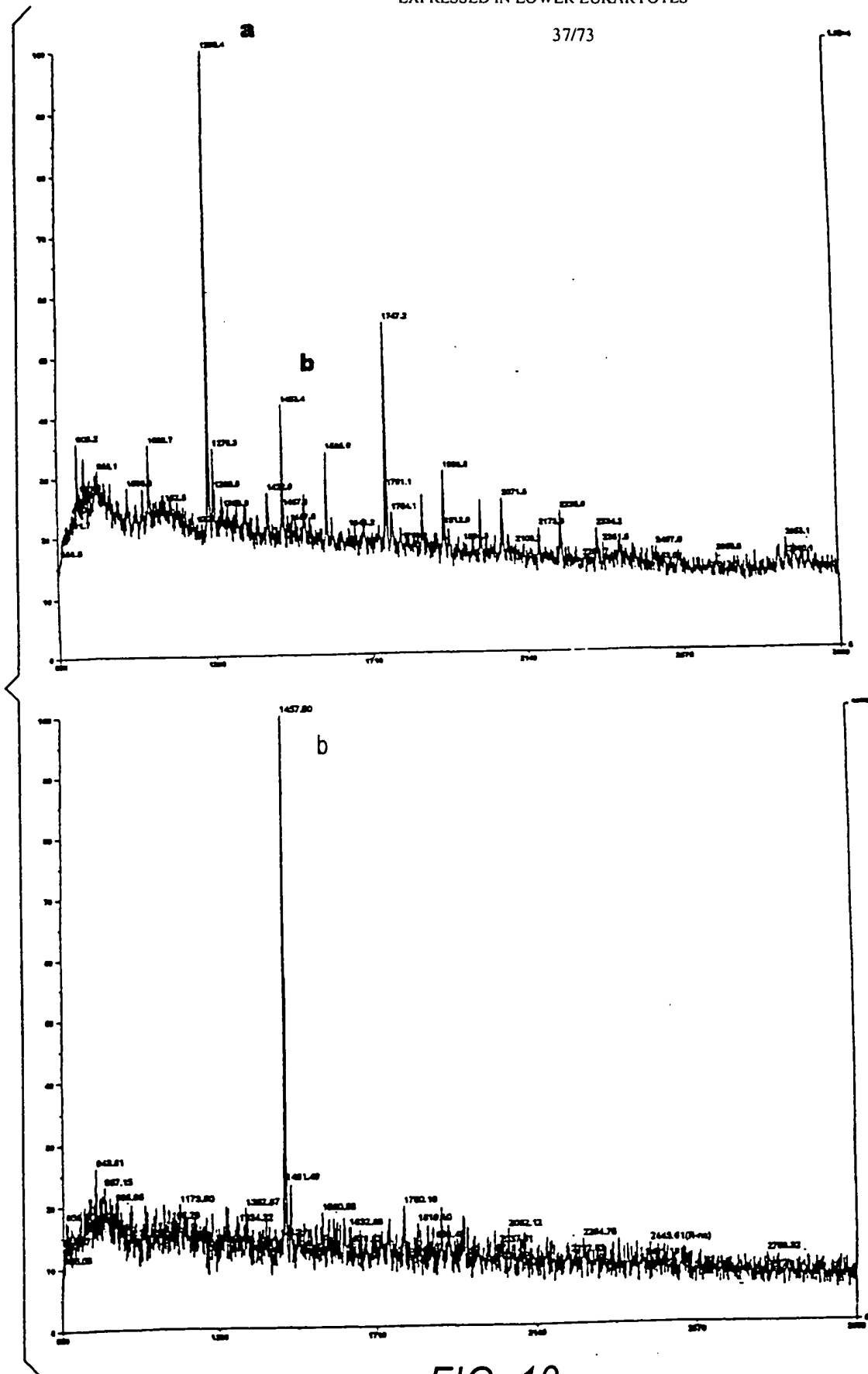
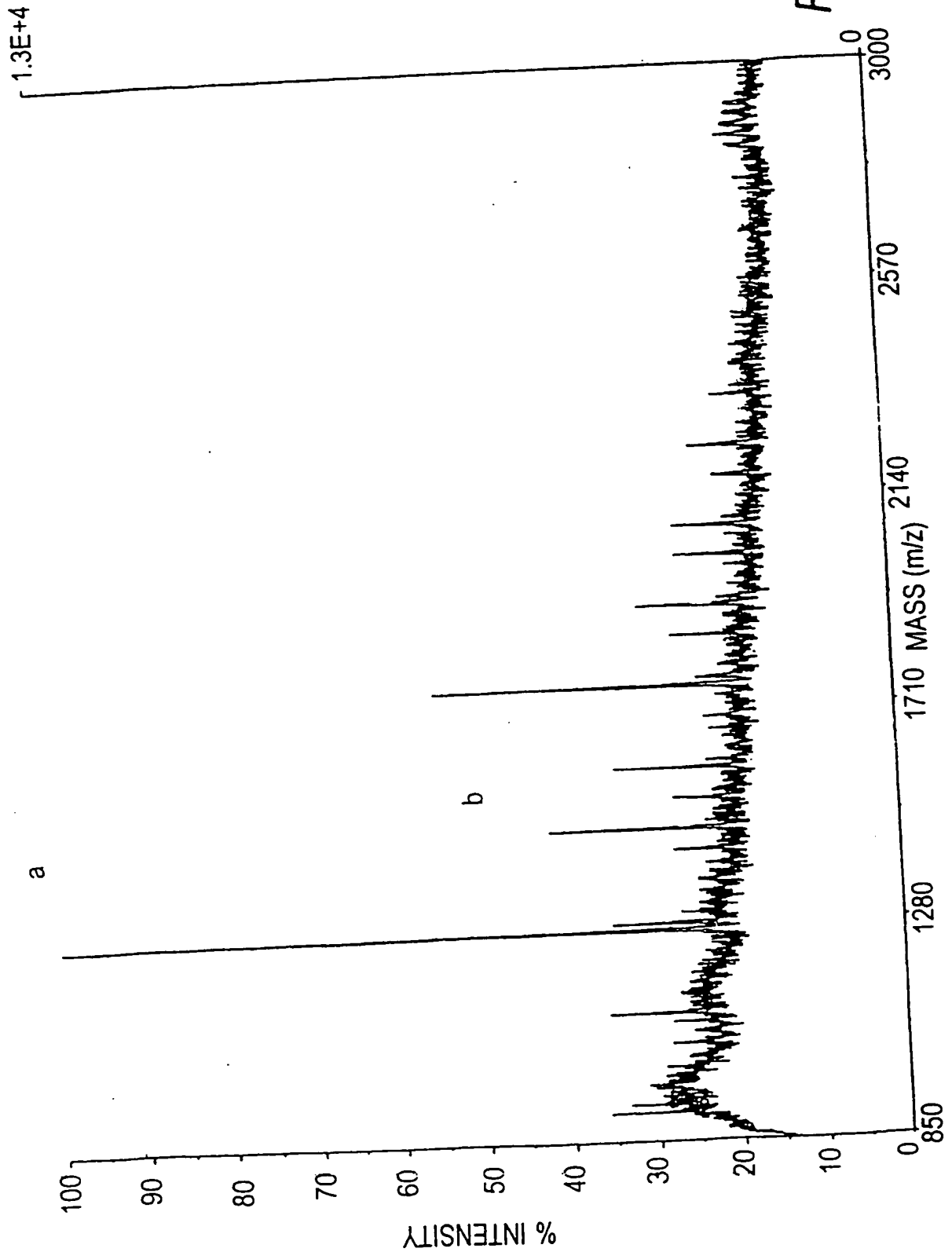


FIG. 9C

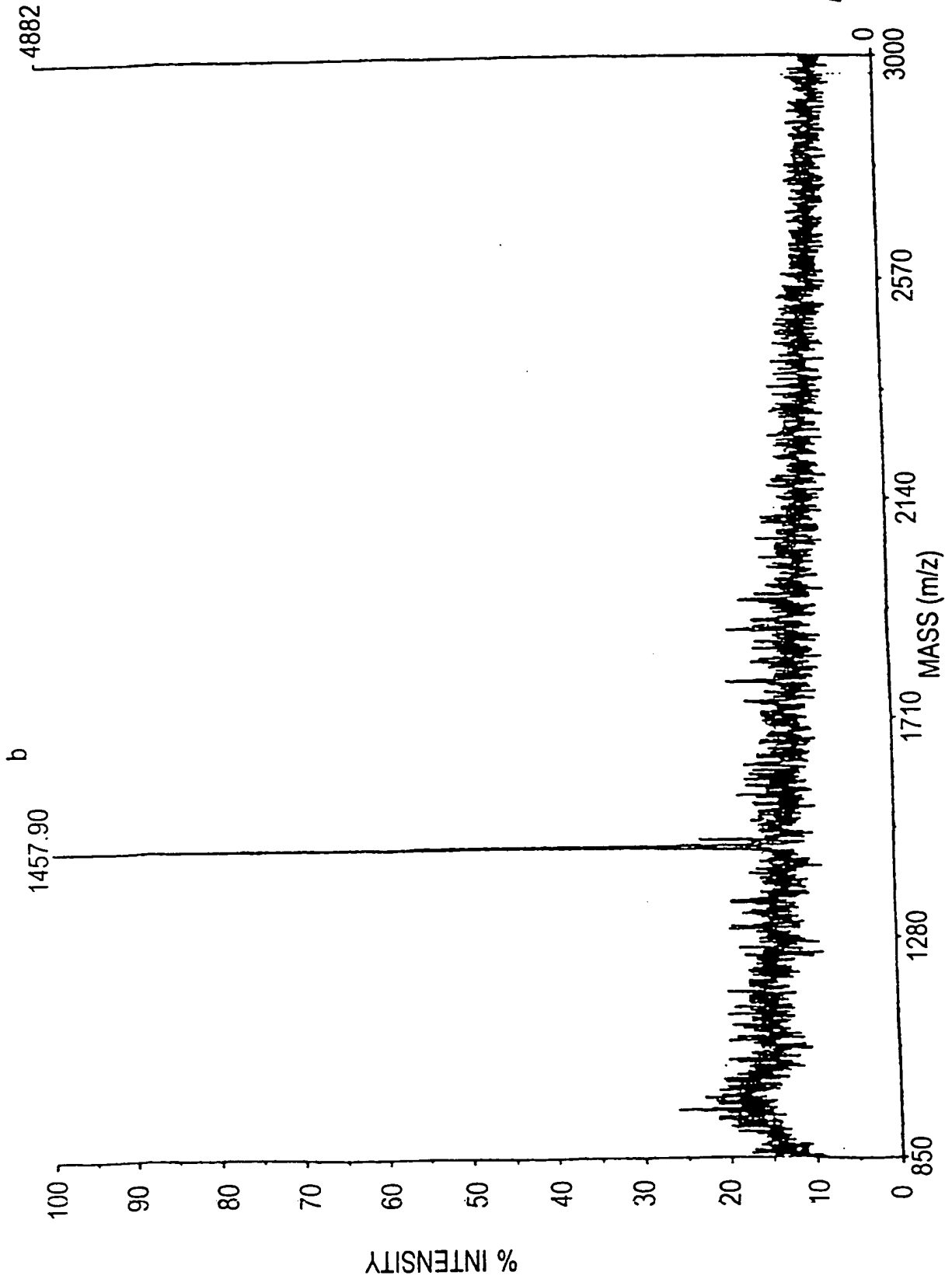


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FIG. 10B



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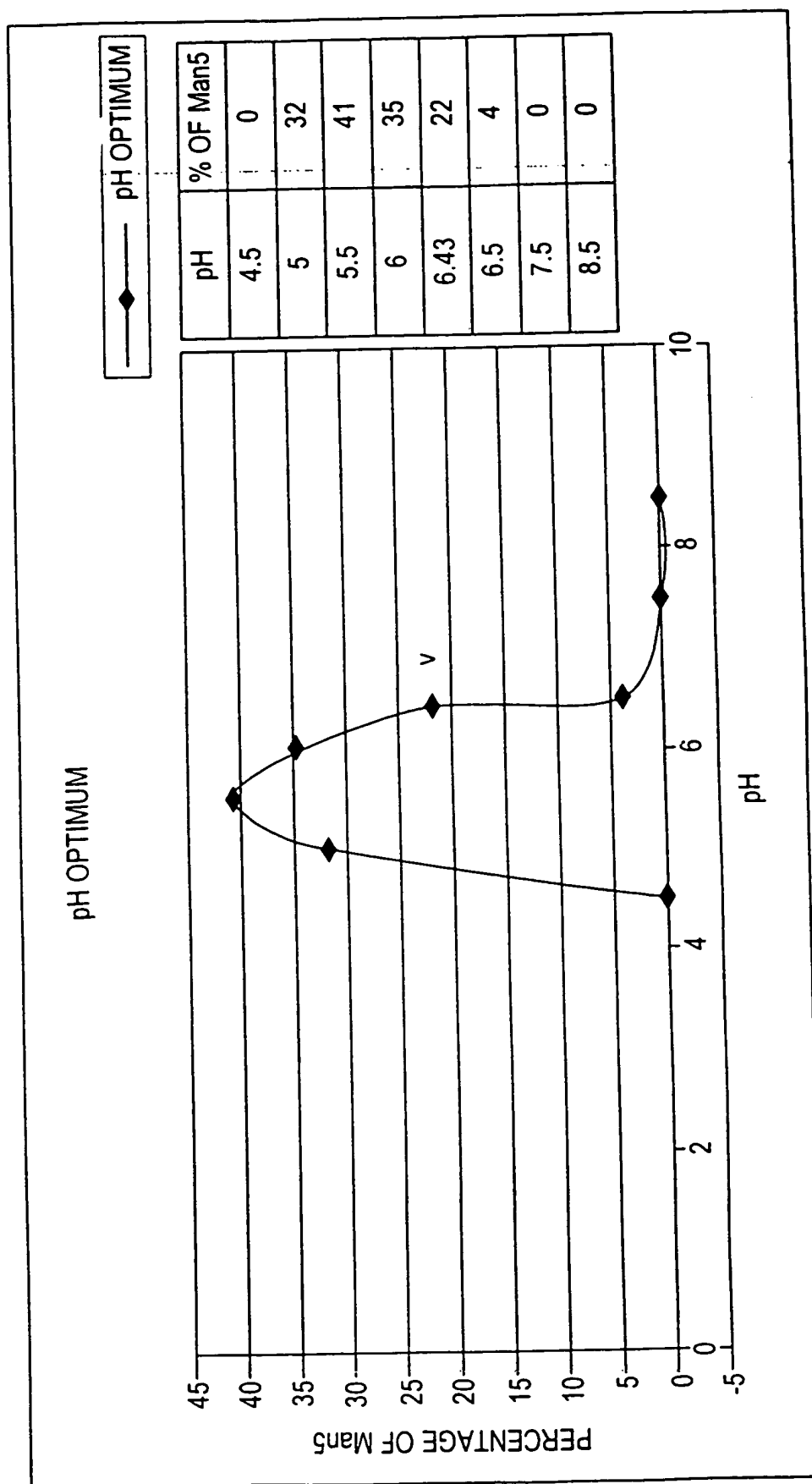


FIG. 11

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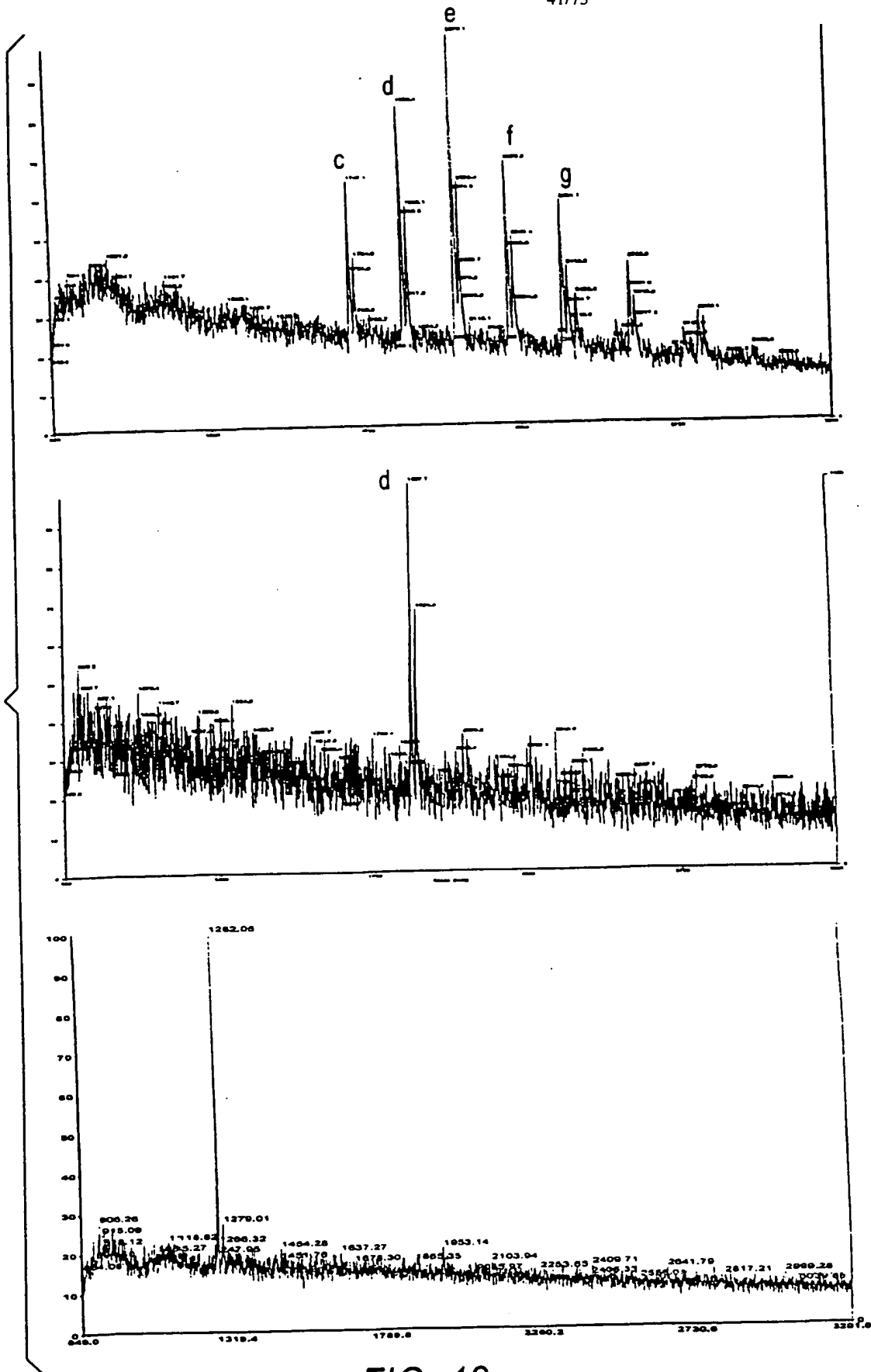
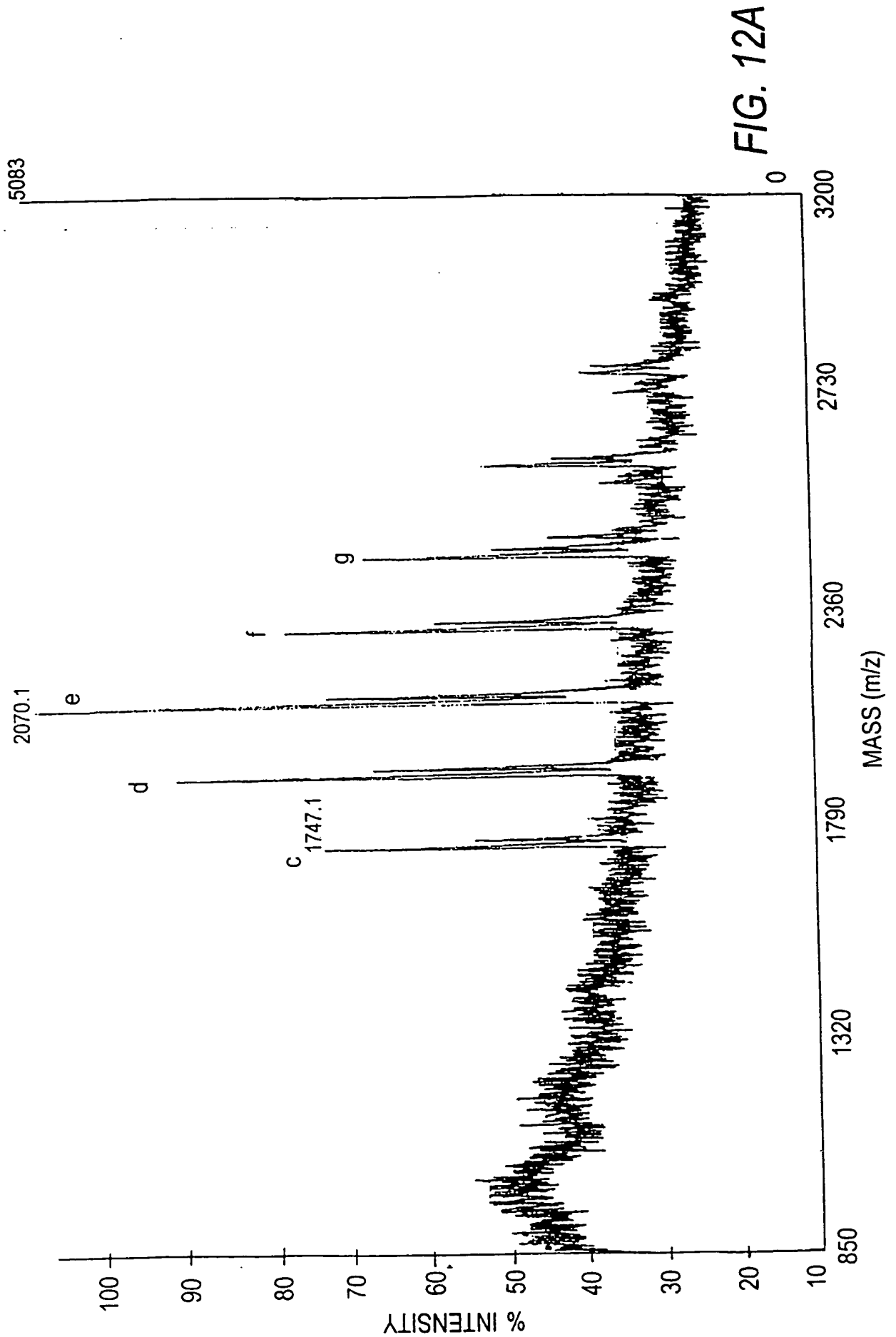
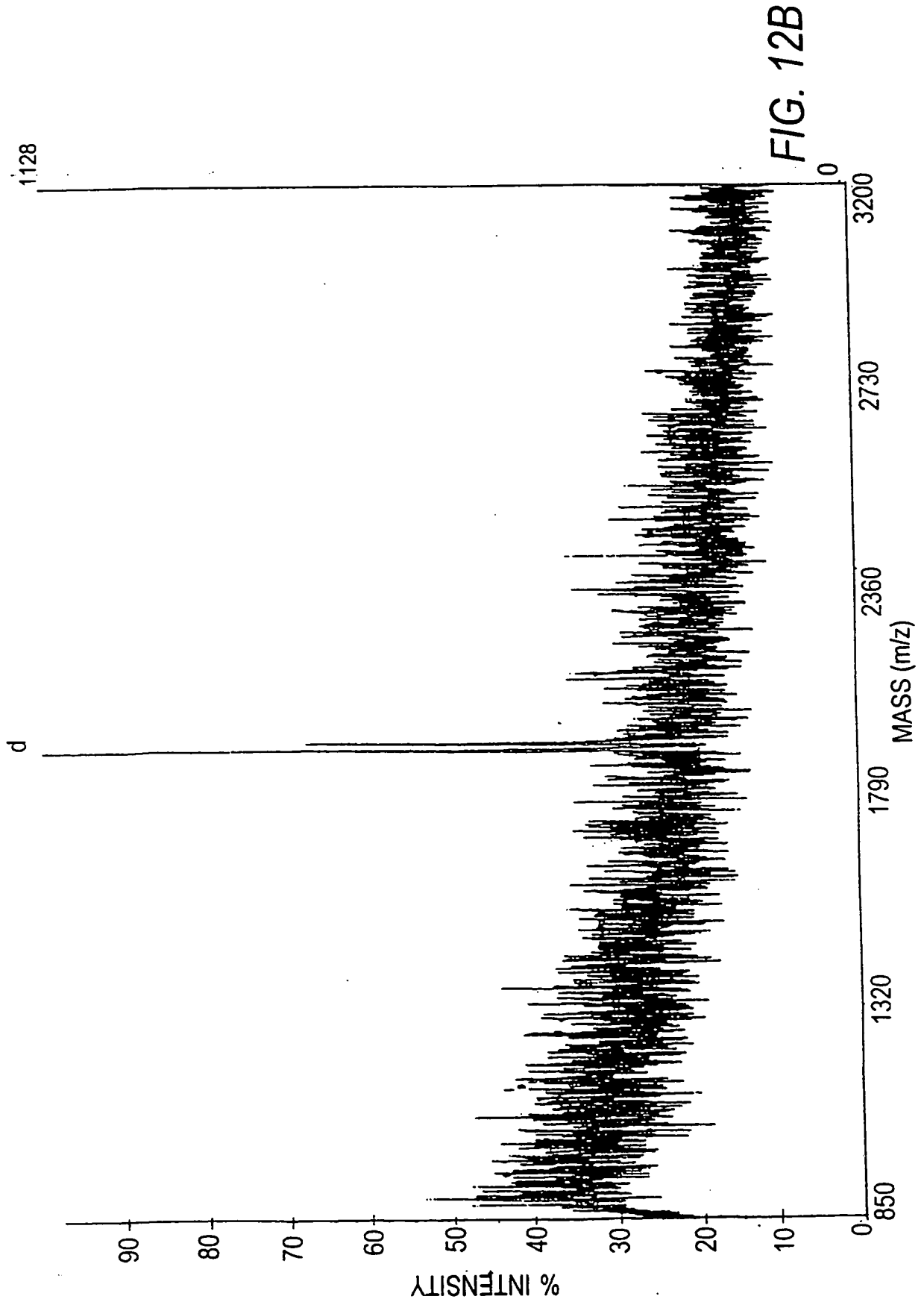


FIG. 12

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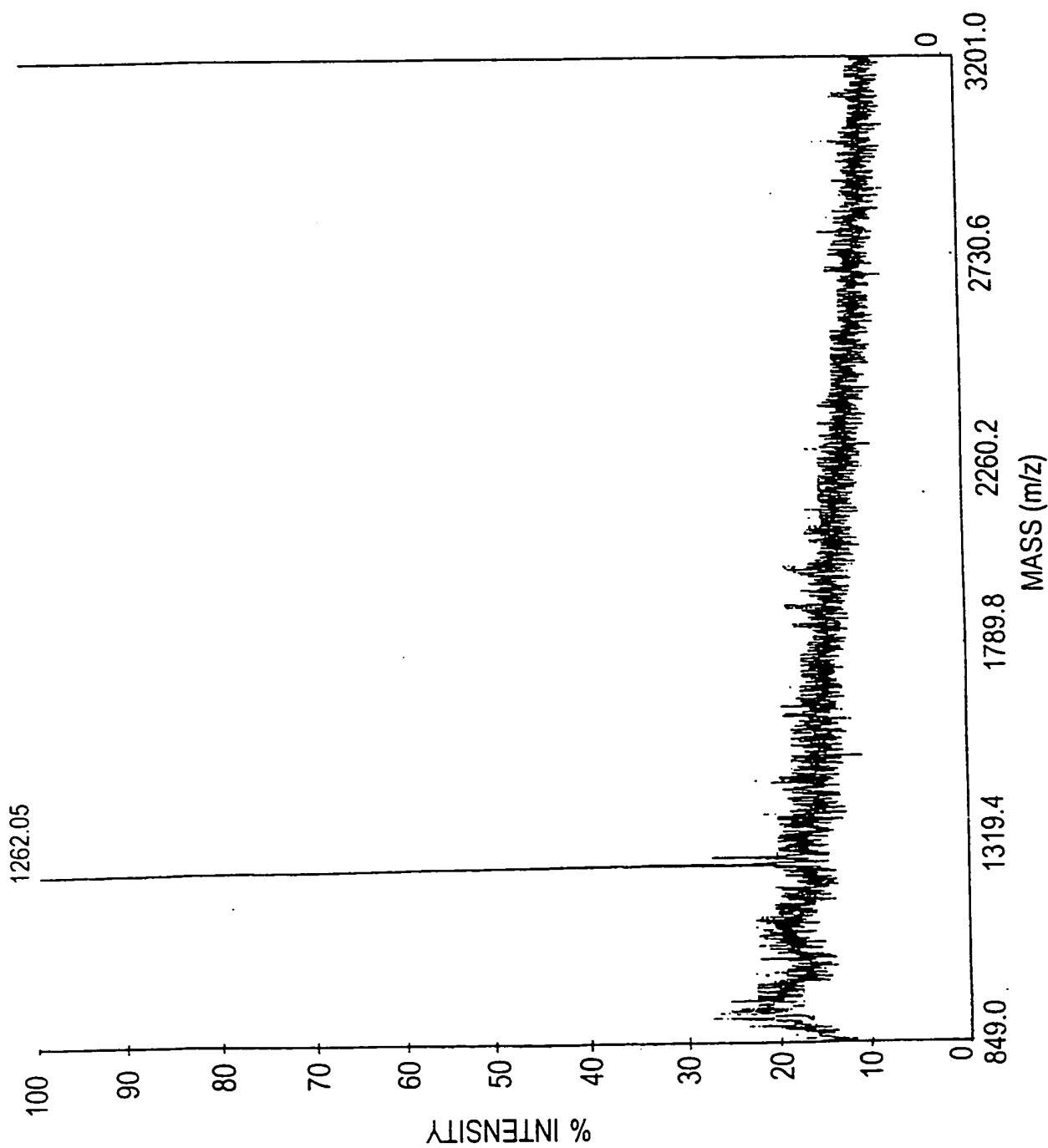


FIG. 12C

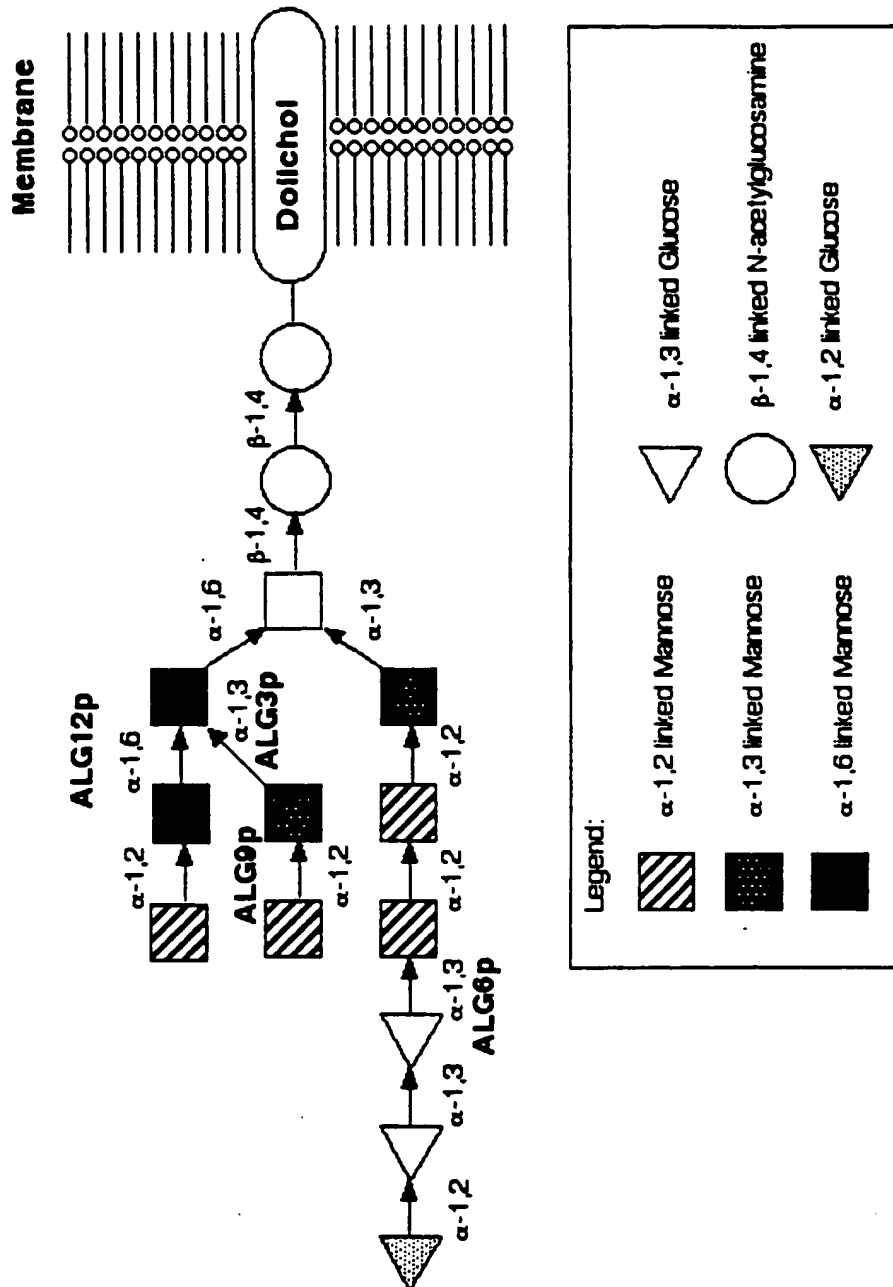


FIG. 13

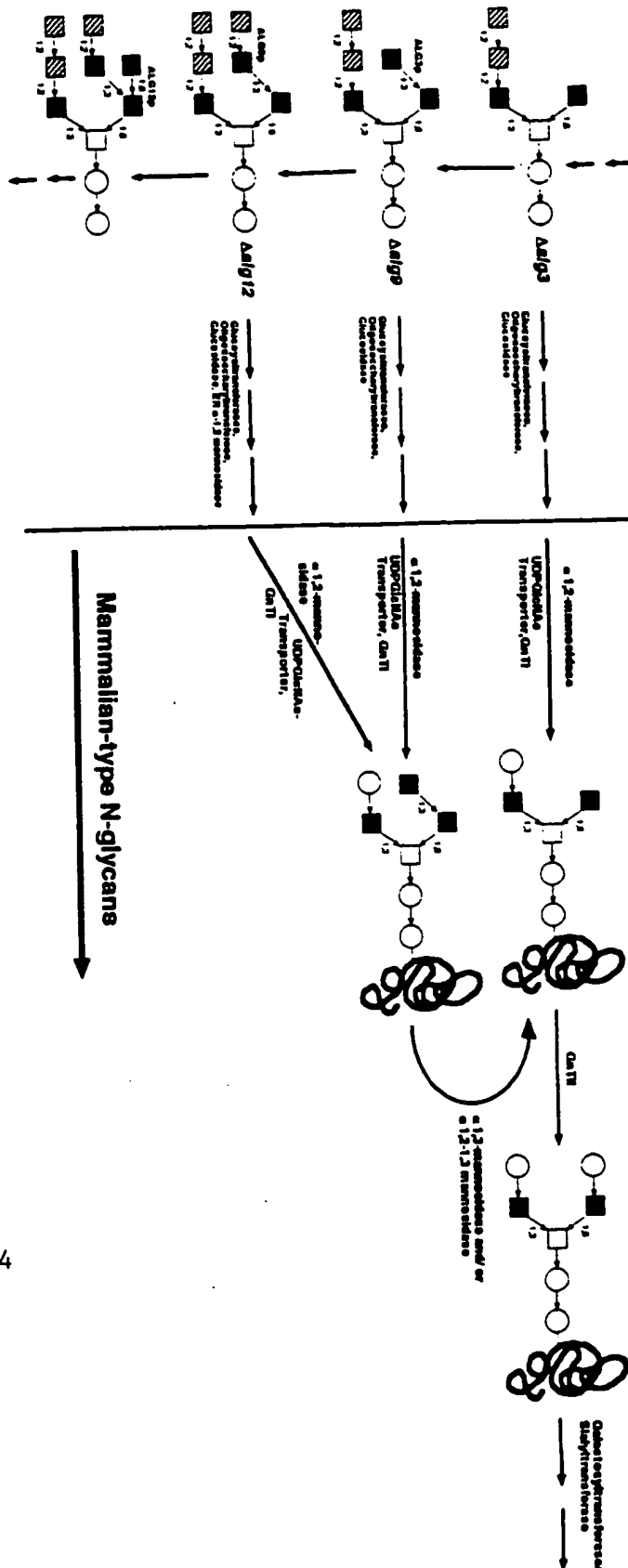


FIG. 14

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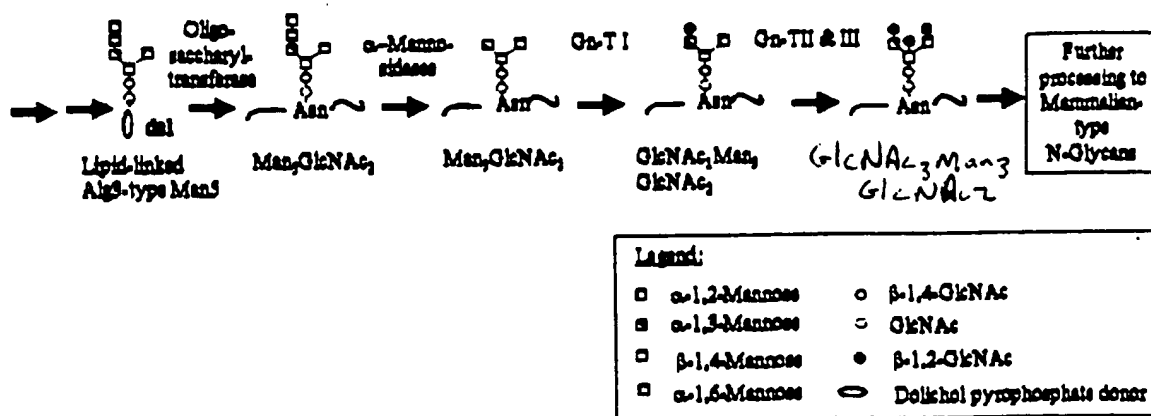


FIG. 15

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ALG3 Blast 05-22-01

Sequences producing significant alignments: (bits) Value

gi 586444 sp P38179 ALG3_YEAST	DOLICHYL-P-MAN:MAN(5)GLCNAC(...797	0.0
gi 3024226 sp Q92685 ALG3_HUMAN	DOLICHYL-P-MAN:MAN(5)GLCNAC...173	7e-43
gi 3024221 sp Q24332 NT56_DROVI	LETHAL(2)NEIGHBOUR OF TID P...145	3e-34
gi 3024222 sp Q27333 NT56_DROME	LETHAL(2)NEIGHBOUR OF TID P...121	3e-27
gi 10720153 sp P82149 NT53_DROME	LETHAL(2)NEIGHBOUR OF TID ...121	5e-27
gi 1707982 sp P40989 GLS2_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 32	2.8
gi 1346146 sp P38631 GLS1_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 31	6.6

Alignments

Yeast

>gi|586444|sp|P38179|ALG3_YEAST DOLICHYL-P-
 MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL MANNOSYLTRANSFERASE
 (DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)
 (HM-1 KILLER TOXIN RESISTANCE PROTEIN)
 Length = 458

Score = 797 bits (2059), Expect = 0.0
 Identities = 422/458 (92%), Positives = 422/458 (92%)

Query: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVIFDCRANLIVMPLLLILFESMLCKI	60
Sbjct: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVIFDCRANLIVMPLLLILFESMLCKI	60
Query: 61	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGM	120
Sbjct: 61	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGM	120
Query: 121	DHVERGQVFFRYLYLLTLALQMACYLLHLPWCVVLACLSKRLHSIYVLRFLNDCFTTL	180
Sbjct: 121	DHVERGQVFFRYLYLLTLALQMACYLLHLPWCVVLACLSKRLHSIYVLRFLNDCFTTL	180
Query: 181	FMVVTVLGAIVASRCHQRPKLKKSALVISATYSMAVSIKMNALLYFPAMMISLFILNDA	240
Sbjct: 181	FMVVTVLGAIVASRCHQRPKLKKSALVISATYSMAVSIKMNALLYFPAMMISLFILNDA	240
Query: 241	NVILTLLDLVAMIAWQVAVVPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFND	300
Sbjct: 241	NVILTLLDLVAMIAWQVAVVPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFND	300
Query: 301	KRFXXXXXXXXXXXXXXXXXVFTRYPRILPDLWSSLCHPLRKNVLANANPAKTIPFVLIASN	360
Sbjct: 301	KRFHLALLISHLIALTTLFVTRYPRILPDLWSSLCHPLRKNVLANANPAKTIPFVLIASN	360
Query: 361	FIGVLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPWIWYVLHEWCWNSYPPNSQXXXXX	420
Sbjct: 361	FIGVLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPWIWYVLHEWCWNSYPPNSQASTLL	420
Query: 421	XXXXXXXXXXXXXXXXXSGSVALAKSHLRTTSSMEKKLN	458
Sbjct: 421	LALNTVLLLLLALTQLSGSVALAKSHLRTTSSMEKKLN	458

FIG. 16-1

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Human

>gi|3024226|sp|Q92685|ALG3_HUMAN DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL
 MANNOSYLTRANSFERASE

(DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)

(NOT56-LIKE PROTEIN)

Length = 438

Score = 173 bits (439), Expect = 7e-43

Identities = 133/396 (33%), Positives = 195/396 (48%), Gaps = 28/396 (7%)

Query: 26 WQDLKDGVRVIFDCRANLIVMPLLLIFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLD 85
 WQ+ R ++ + R L+V L L E + +I +VAYTEID+KAYM ++E + ++
 Sbjet: 29 WQER----RLLLREPRYTLLVAACLCLAEVGITFWVIHRVAYTEIDWKAYMAEVEGV-IN 83

Query: 86 GMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACY 145
 G DY+Q+ G TGPLVYPAG V I+ +Y+ T + Q F LYL TL L Y
 Sbjet: 84 GTYDYTLQGDGTGPLVYPAGFVYIFMGLYYATSRGTDIRMAQNI FAVLYLATLLLVFLIY 143

Query: 146 Y-LLHLPWC-VVLACL SKRLHSIYVLRFLNDCFTTLFMVVTVLGAIVASRCHQRPKLKK 203
 + +PP+ + C S R+HSI+VLRFLND + + +L + QR
 Sbjet: 144 HQTKVPPFVFFFMCCASYRVHSIFVLRFLNDP-----VAMVLLFLSINLLLAQRWGWG- 197

Query: 204 SLALVISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPF 263
 +S+AVS+KMN LL+ P ++ L L L + A + QV + +PF
 Sbjet: 198 -----CCFFSLAVSVKMNVLFLFAPGLLFLLLTQFGFRGALPKLGICAGL--QVVLGLPF 249

Query: 264 LRSFPQOYLHCAFNFGRKFMYSINWQMMDEEAFNDKRFXXXXXXXXXXXXXXXXXVTRY 323
 L P YL +F+ GR+F++ W++NW+ + E F + F + R+
 Sbjet: 250 LLENPSGYLSRSFDLGRQFLFWHTVNWRFLEALFLHRAFLALHTAHLTLLLLFALCRW 309

Query: 324 PRILPDLWSSLCHPLRKNVLANPACTIPFVLIASNFIGVLFSLHYQFLSWYHWTLP 383
 R + S L P ++ I L SNFIG+ FSRLHYQF WY TLP
 Sbjet: 310 HRTGESILSLLRDPSCRKVPQPLTPNQIVSTLFTSNFIGICFSRLHYQFVWYFHTLP 369

Query: 384 ILIF-----WSGMPFFVGPIWYVLHEWCWNSYPPNS 414
 L++ W + + + E WN+YP S
 Sbjet: 370 YLLWAMPARWLTHLLRLLVLGLI--ELSWNTYPSTS 403

Drosophila Vi

>gi|3024221|sp|Q24332|NT56_DROVI LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT58)
 Length = 526

Score = 145 bits (366), Expect = 3e-34

Identities = 103/273 (37%), Positives = 157/273 (56%), Gaps = 17/273 (6%)

Query: 33 VRYVIFDCRANLIVMPLLLIFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQ 92
 ++Y+ F+ A IV L++L E+++ ++I++V YTEID+KAYM++ E L+G +YS
 Sbjet: 34 IKYLAFEPAALPIVSVLIVLAEAVINVLIQRPVTEIDWKAYMQECEGF-LNGTTNYSL 92

Query: 93 VSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLH-LP 151
 + G TGPLVYPA V IY +Y+LT +V Q F +YLL + L + Y +P
 Sbjet: 93 LRGDTGPLVYPAAFVYIYSGLYYLTGQGTNVRLAQYIFACIYLLQCLVLRLYTKSRKVP 152

Query: 152 PWCVVLACL-SKRLHSIYVLRFLNDCFTTLFMVVTVLGAIVASRCHQRPKLKKSALVIS 210
 P+ +VL+ S R+HSIYVLRFLND L +L A + QR L S
 Sbjet: 153 PYVLVLSAFTSYRIHSIYVLRFLNDPVAI-----LLYAALNLFQDQRTLG-----S 200

Query: 211 ATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQ 270
 YS+AV +KMN + A + LF L + V+ TL+ L Q+ + PFLR+ P +
 Sbjet: 201 ICYSLAVGVKMN--ILLFAPALLLFYLANLGLRTLVLQTLCAVLQLFIGAPFLRTHPME 258

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Query: 271 YLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303
 YL +F+ GR F ++W++N++ + +E F + F
 Sbjct: 259 YLRGSFDLGRIFEHKWTVNYRFLSKELFEQREF 291

Score = 53.3 bits (127), Expect = 1e-06
 Identities = 31/62 (50%), Positives = 41/62 (66%), Gaps = 6/62 (9%)

Query: 352 IPFVLIASNFIGVLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLH--EWCWNS 409
 +PF L NFIGV +RSLHYQF WY +LP L+ WS P+ +G + +L E+CWN+
 Sbjct: 412 LPFFL--CNFIGVACARSLHYQFYIWFHSLPYLV-WS-TPYSLGVRYLILGIEYCWN 467

Query: 410 YP 411
 YP
 Sbjct: 468 YP 469

Drosophila melanogaster

>gi|3024222|sp|Q27333|NT56_DROME LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT56)
 (NOT45)

Length = 510

Score = 121 bits (305), Expect = 3e-27
 Identities = 96/272 (35%), Positives = 154/272 (56%), Gaps = 17/272 (6%)

Query: 34 RYVIFDCRANLIVMPLLLFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQV 93
 +Y++ + A IV ++L E ++ ++I++V YTEID+ AYM++ E L+G +YS +
 Sbjct: 36 KYLLLEPAALPIVGLFVLLAELVINVVVVIQRPVYTEIDWVAYMQECEGF-LNGTTNYSLL 94

Query: 94 SGGTGPLVYPAGHVLIYKMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLH-LPP 152
 G TGPLVYPA V IY +Y++T +V Q F +YLL LAL + Y +PP
 Sbjct: 95 RGD TGPLVYPAFVYIYSALYYVTSHGTVNRLAQYIFAGIYLLQLALVLRLYSKSRKVPP 154

Query: 153 WCVVLACL-SKRLHSIYVLRFLFNDCTTLFMVVTVLGAIVASRCHQRPKLKSLALVISA 211
 + +VL+ S R+HSIYVLRFLFND + V +L A + +R L S
 Sbjct: 155 YVLVLSAFTSYRIHSIYVLRFLFNDP-----VAVLLLYAALNLFDRRWTLG-----ST 202

Query: 212 TYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVVPFLRSFPQY 271
 +S+AV +KMN + A + LF L + ++ T+L L Q+ + PFL + P +Y
 Sbjct: 203 FFSLAVGVKMN--ILLFAPALLLFYLANLGLLRTILQLAVCGVIQLLLGAPFLTHPVEY 260

Query: 272 LHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303
 L +F+ GR F ++W++N++ + + F ++ F
 Sbjct: 261 LRGSFDLGRIFEHKWTVNYRFLSRDVFENRTF 292

Score = 49.4 bits (117), Expect = 2e-05
 Identities = 27/60 (45%), Positives = 35/60 (58%), Gaps = 2/60 (3%)

Query: 352 IPFVLIASNFIGVLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYP 411
 +PF L N +GV SRSLHYQF WY +LP L + + V + L E+CWN+YP
 Sbjct: 407 LPFFL--CNLVGVACSRSLHYQFYVWYFHSPLYLAWSTPYSLGVRCILGLIEYCWN 464

FIG. 16-3

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Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 28883317
Number of Sequences: 96469
Number of extensions: 1107545
Number of successful extensions: 2870
Number of sequences better than 10.0: 16
Number of HSP's better than 10.0 without gapping: 5
Number of HSP's successfully gapped in prelim test: 11
Number of HSP's that attempted gapping in prelim test: 2839
Number of HSP's gapped (non-prelim): 23

length of query: 458
length of database: 35,174,128
effective HSP length: 45
effective length of query: 413
effective length of database: 30,833,023
effective search space: 12734038499
effective search space used: 12734038499
T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.8 bits)
S2: 67 (30.4 bits)

FIG.16-4

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S. cerevisiae ALG3

ATGGAAGGTGAACAGTCTCCGCAAGGTGAAAAGTCTCTGCAAAGGAAGC
AATTTGTCAGACCTCCGCTGGATCTGTGGCAGGATCTCAAGGACGGTGTG
CGCTACGTGATCTTCGATTGTAGGGCCAATCTTATCGTTATGCCCCTTTTG
ATTTTGTTGAAAGCATGCTGTGCAAGATTATCATTAAGAAGGTAGCTTAC
ACAGAGATCGATTACAAGGCGTACATGGAGCAGATCGAGATGATTCAGCT
CGATGGCATGCTGGACTACTCTCAGGTGAGTGGTGGAAACGGGCCCCGCTGG
TGTATCCAGCAGGCCACGTCTTGATCTACAAGATGATGTACTGGCTAACA
GAGGGAATGGACCACGTTGAGCGCGGGCAAGTGTTTTTCAGATACTTGTA
TCTCCTTAACTGGCGTTACAAATGGCGTGTTACTACCTTTTACATCTACC
ACCGTGGTGTGTGGTCTTGGCGTGCCTCTCTAAAAGATTGCACTCTATTTA
CGTGCTACGGTTATTCAATGATTGCTTCACTACTTTGTTTATGGTCGTCACG
GTTTTGGGGGCTATCGTGGCCAGCAGGTGCCATCAGCGCCCCAAATTAAA
GAAGTCCCTTGCGCTGGTGTATCTCCGCAACATACAGTATGGCTGTGAGCA
TTAAGATGAATGCGCTGTTGTATTTCCCTGCAATGATGATTTCTCTATTCAT
CCTTAATGACGCGAACGTAATCCTTACTTTGTTGGATCTCGTTGCGATGAT
TGCATGGCAAGTCGCAGTTGCAGTGCCCTTCCCTGCGCAGCTTTCCGCAACA
GTACCTGCATTGCGCTTTTAATTTTCGGCAGGAAGTTTATGTACCAATGGAG
TATCAATTGGCAAATGATGGATGAAGAGGCTTTCAATGATAAGAGGTTCC
ACTTGGCCCTTTTAATCAGCCACCTGATAGCGCTCACCACACTGTTTCGTCA
CAAGATACCCTCGCATCCTGCCCCGATTTATGGTCTTCCCTGTGCCATCCGC
TGAGGAAAAATGCAGTGCTCAATGCCAATCCCGCCAAGACTATTCCATTC
GTTCTAATCGCATCCAACCTTCATCGGCGTCCTATTTTCAAGGTCCCTCCAC
TACCAGTTTCTATCCTGGTATCACTGGACTTTGCCTATACTGATCTTTTGGT
CGGGAATGCCCTTCTTCGTTGGTCCCATTTGGTACGTCTTGCACGAGTGGT
GCTGGAATTCCTATCCACCAAACTCACAAGCAAGCACGCTATTGTTGGCA
TTGAATACTGTTCTGTTGCTTCTATTGGCCTTGACGCAGCTATCTGGTTCGG
TCGCCCTCGCCAAAAGCCATCTTCGTACCACCAGCTCTATGGAAAAAAG
CTCAACTGA

S. cerevisiae Alg3p

MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLL
FESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAG
HVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLHLPWCV
VLACLSKRLHSIYVLRLFNDCFTTLFMVVTVLGAIVASRCHQRPKLKSLALV
ISATYSMAVSIMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVA
VPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRFHLALLISHL
IALTTLFVTRYPRILPDLWSSLCHPLRKNVNLNANPAKTIPFVLASNFIGVLFS
RSLHYQFLSWYHWTLPIIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQASTL
LLALNTVLLLLLALTQLSGSVALAKSHLRTTSSMEKKLN

FIG. 17

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P. pastoris ALG3

ATGCCTCCGATAGAGCCAGCTGAAAGGCCAAAGCTTACGCTGAAAAATGT
TATCGGTGATCTAGTGGCTCTTATTCAAACGTTTATTTAACCCAGATTTT
AGTGTCTTCGTTGCACCTCTTTTATGGTTAGCTGATTCCATTGTTATCAAGG
TGATCATTGGCACTGTTTCCTACACAGATATTGATTTTTCTTCATATATGCA
ACAAATCTTTAAAATTCGACAAGGAGAATTAGATTATAGCAACATATTTG
GTGACACCGGTCCATTGGTTTACCCAGCCGGCCATGTTTCATGCTTACTCAG
TACTTTCGTGGTACAGTGATGGTGGAGAAGACGTCAGTTTCGTTCAACAA
GCATTTGGTTGGTTATACCTAGGTTGCTTGTACTATCCATCAGCTCCTACT
TTTTCTCTGGCTTAGGGAAAATACCTCCGGTTTATTTTGTGTTTGTGGTAGC
GTCCAAGAGACTGCATTCAATATTTGTATTGAGACTCTTCAATGACTGTTT
AACAACATTTTTGATGTTGGCAACTATAATCATCCTTCAACAAGCAAGTAG
CTGGAGGAAAGATGGCACAACCTATTCCATTATCTGTCCCTGATGCTGCAG
ATACGTACAGTTTAGCCATCTCTGTAAAGATGAATGCGCTGCTATACCTCC
CAGCATTCTACTACTCATATATCTCATTGTGACGAAAATTTGATTAAAG
CCTTGGCACCTGTTCTAGTTTTGATATTGGTGCAAGTAGGAGTCGGTTATT
CGTTCATTTTACCGTTGCACTATGATGATCAGGCAAATGAAATTCGTTCTG
CCTACTTTAGACAGGCTTTTGAAGTTTGTGCGCAATTTCTTTATAAGTGGA
CGGTTAATTGGCGCTTTTGTAGCCAAGAACTTTCAACAATGTCCATTTTC
ACCAGCTCCTGTTTGCTCTCCATATTATTACGTTAGTCTTGTTTCATCCTCAA
GTTCTCTCTCCTAAAAACATTGGAAAACCGCTTGGTAGATTTGTGTTGGA
CATTTTCAAATTTTGGGAAGCCAACCTTATCTCCAACCAATATTATCAACGA
CCCAGAAAGAAGCCCAGATTTTGTGTTACACCGTCATGGCTACTACCAACTT
AATAGGGGTGCTTTTTGCAAGATCTTTACACTACCAGTTCCTAAGCTGGTA
TGCGTTCTCTTTGCCATATCTCCTTTACAAGGCTCGTCTGAAGTTTATAGCA
TCTATTATTGTTTATGCCGCTCACGAGTATTGCTGGTTGGTTTTCCAGCTA
CAGAACAAAGTTCCGCGTTGTTGGTATCTATCTTACTACTTATCCTGATTC
TCATTTTTACCAACGAACAGTTATTTCTTCTCAATCGGTCCCTGCAGAAA
AAAAGAATACATAA

P. pastoris Alg3p

MPPIEPAERPKLTLKNVIGDLVALIQNVLFNPDFS VFVAPLLWLADSVIKVIIG
TVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYS
DGGEDVSFVQQA FGWLYLGCLLLSISSYFFSGLGKIPVYFVLLVASKRLHSIF
VLR LFNDCLTTF LMLATIHLQQASSWRKDGTIPLSVPAADTYS LAISVKMN
ALLYLPAFLLLIYLICDENLIKALAPVLVLILVQVG VGYSFILPLHYDDQANEIR
SAYFRQAFDFS RQFLYKWTVNWRFLS QETFNNVHFHQLLFALHIITLVLFILKF
LSPKNIGKPLGRFVLDIFKFWKPTLSPTNIINDPERSPDFVYTVMATTNLIGVLF
ARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWLVPATEQSSAL
LVSILLILILIFTNEQLFPSQSVP AEKKNT

FIG. 18

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P. pastoris ALG3 BLAST

Sequences producing significant alignments: (bits) Value

qi 586444 sp P38179 ALG3 YEAST Dolichyl-P-Man:Man(5)GlcNAc(...	228	2e-58
qi 12802365 qb AAK07848.1 AF309689 10 putative NOT-56 manno...	212	8e-54
qi 984725 qb AAA75352.1 ORF 1	206	4e-52
qi 7492702 pir T39084 probable mannosyltransferase - fissi...	176	8e-43
qi 16226531 qb AAL16193.1 AF428424 1 At2g47760/F17A22.15 [A...	164	2e-39
qi 25367230 pir B84919 Not56-like protein [imported] - Ara...	164	3e-39
qi 25814791 emb CAB70171.2 Hypothetical protein K09E4.2 [C...	161	2e-38
qi 17535001 ref NP 496950.1 Putative plasma membrane membr...	160	3e-38
qi 1654000 emb CAA70220.1 Not56-like protein [Homo sapiens...	155	2e-36
qi 13279206 qb AAH04313.1 AAH04313 Unknown (protein for IMA...	154	2e-36
qi 22122365 ref NP 666051.1 hypothetical protein MGC36684 ...	150	3e-35
qi 21292031 qb EAA04176.1 agCP3388 [Anopheles gambiae str...	120	4e-26
qi 1780792 emb CAA71167.1 lethal(2)neighbour of tid [Droso...	114	3e-24

Alignments

S. cerevisiae

Score = 228 bits (580), Expect = 2e-58
 Identities = 154/429 (35%), Positives = 229/429 (53%), Gaps = 37/429 (8%)

Query: 9 RPKLTLKNVIGDLVALIQNVLFNPDFSVFVAPLLWLADSIKVIIGTVSYTDIDFSSYM 68
 RP L L DL ++ V+F+ ++ V PLL L +S++ K+II V+YT+ID+ +YM
 Sbjct: 20 RPPLDLWQ---DLKDGVRVYIFDCRANLIVMPLILFESMLCKIIKKVAYTEIDYKAYM 76

Query: 69 QQIFKIR-QGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYSDGGEDVSFVQQAFGWLYLG 127
 +QI I+ G LDYS + G TGPLVYPAGHV Y ++ W ++G + V Q F +LYL
 Sbjct: 77 EQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFRYLYLL 136

Query: 128 CLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIFVLRFLFNDCLTTFMLLATI---IILQ 184
 L L ++ Y+ L +PP VL SKRLHSI+VLRFLFNDCL TT M+ T+ I+
 Sbjct: 137 TLALQMACYY---LLHLPPWCVVLAACLSKRLHSIYVLRFLFNDCLTTFMLVVTVLGAIVAS 193

Query: 185 QASSWRKDGTTIPLSVDAADTYSLSIVKMNXXXXXXXXXXXXXXXXXCDENLIKALAPXX 244
 + K ++ L + + TYS+A+S+KMN D N+I L
 Sbjct: 194 RCHORPKLKKSLALVI---SATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLV 250

Query: 245 XXXXXXXXXXXXSYFILPLHYDDQANEIRSAYFRQAFDFSRQFLYKWTNVNWRFLSQETFNNV 304
 F+ Y AF+F R+F+Y+W++NW+ + +E FN+
 Sbjct: 251 AMIAWQVAVAVPFL-----RSFPQQYLHCAFNFGRKFMYSINWQMMDEEAFNDK 301

Query: 305 HFHQLLFALHIITL-VLFILKFLSPKNIGKPLGRFVLDIFKFWKPTLSPTNIIN-DPERS 362
 FH L H+I L LF+ ++ R + D++ L ++N +P ++
 Sbjct: 302 RFHLALLISHLIAITLTFVTRY-----PRILPDLWSSSLCHPLRKNVLANANPAKT 351

Query: 363 PDFVYTVMATNLIGVLFARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWL 422
 F V+ +N IGVLF+RSLHYQFLSWY ++LP L++ + + F I Y HE+CW
 Sbjct: 352 IPF---VLIASNFIVGLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPVIWVYLHEWCWN 408

Query: 423 VFPATEQSS 431
 +P Q+S
 Sbjct: 409 SYPPNSQAS 417

FIG. 19-1

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Neurospora crassa

Score = 212 bits (540), Expect = 8e-54
 Identities = 140/400 (35%), Positives = 212/400 (53%), Gaps = 29/400 (7%)

Query: 35 SVFVAPLLWLADSIKVIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYP 94
 S + P L+L D+++ +II V YT+ID+++YM+Q+ +I GE DY+ + G TGPLVYP
 Sbjct: 33 SKLIPPALFLVDALLCGLIIWKVPYTEIDWAAAYMEQVSQILSGERDYTKVRGGTGPLVYP 92

Query: 95 AGHVHAYSVLSWSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVA 154
 A HV+ Y+ L +D G ++ QQ F LY+ L + + Y+ K PP F LL
 Sbjct: 93 AAHVYIYTGLYHLLTDEGRNILLAQQLFAGLYMVT LAVVMGCYW---QAKAPPYLFPLLTL 149

Query: 155 SKRLHSIFVLRFLNDCLTTFMLATIIILQQASSWRKDGTTIPLSVPAADTYSLAISVK 214
 SKRLHSIFVLR FNDC + I Q+ +W+ A Y+L + VK
 Sbjct: 150 SKRLHSIFVLRFCFNDCAFVLFWLAIFFQFQ-RNQWQ-----GALLYTLGLGVK 197

Query: 215 MNXXXXXXXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPHYDDQANEIRSAY 274
 M + + L F+ HY + Y
 Sbjct: 198 MTLTLLSLPAVGIVLFLGSG-SFVTTLQLVATMGLVQILIGVPFL--AHYPTE-----Y 247

Query: 275 FRQAFDFSQFLYKWTNVNRFSLQETFNNVHFHQLLALHIITLVLFIL-KFLSPKNIGK 333
 +AF+ SRQF +KWTNVNRF+ +E F + F L ALH++ L +FI +++ P K
 Sbjct: 248 LSRAFELSRQFFFKWTNVNRFVGEIIFLSKGFALTLLALHVLVLGIFITTRWIKPAR--K 305

Query: 334 PLGRFVLDFKFWKPTLS-PTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWY 392
 L + + + KP L+ P + + P ++ T + + N +G+LFARSLHYQF ++
 Sbjct: 306 SLVQLISPVLLAGKPLTVPEHRAARDVTPRYIMTTILSANAVGLLFARSLHYQFYAYV 365

Query: 393 AFSLPYLLYKARLNFIASIIIVYAAHEYCWLVPFATEQSSA 432
 A+S P+LL++A L+ + +++A HE+ W VFP+T SSA
 Sbjct: 366 AWSTPFLWRAGLHPVLVYLLWAVHEWAWNVFPSTPASSA 405

Schizosaccharomyces pombe

Score = 176 bits (445), Expect = 8e-43
 Identities = 132/390 (33%), Positives = 194/390 (49%), Gaps = 35/390 (8%)

Query: 42 LWLADSIKVIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAY 101
 L L + + II V YT+ID+ +YM+Q+ GE DY++ G TGPLVYP GHV Y
 Sbjct: 30 LLLLEIPFVFAIISKVPYTEIDWIAAYMEQVNSFLLGERDYKSLVGCTGPLVYPGGHVFLY 89

Query: 102 SVLSWSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSI 161
 ++L + +DGG ++ Q F ++Y + +I Y F + + P +VLL+ SKRLHSI
 Sbjct: 90 TLLYVLTGDTNIVRAQYIFAFVYW--ITTAIVGYLFK-IVRAPFYIYVLLIILSKRLHSI 146

Query: 162 FVLRLFNDCLTTFMLATIIILQQASSWRKDGTTIPLSVPAADTYSLAISVKMNXXXXX 221
 F+LRLFND + L + I+ W + A+ S+A SVKM+
 Sbjct: 147 FILRLFNDGFNS-LFSSLFILSSCKKKWVR-----ASILLSVACSVKMSSLLYV 194

Query: 222 XXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPHYDDQANEIRSAYFRQAFDF 281
 L++ L P + + + +Y+ QAFDF
 Sbjct: 195 PAYLVL-----LLQILGPKKTWMHIFVIIIVQILFSIPF----LAYFWSYWTQAFDF 242

Query: 282 SRQFLYKWTNVNRFSLQETFNNVHFHQLLALHIITLVLFILKFLSPKNIGKPLGRFVLDF 341
 R F YKWTNVNRF+ + F + F + LH+ LV F K + + P
 Sbjct: 243 GRAFDYKWTNVNRFIPRSIFESTSFSTSILFLHVALVAFTCKHWNKLSRATP----- 295

Query: 342 IFKFWKPTLSPTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWYAFSLPYLLY 401
 F L+ + +P+F++T +AT+NLIG+L ARSLHYQF +W+A+ PYL Y

FIG. 19-2

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Sbjct: 296 -FAMVNSMLTLKPLPKLQLATPNFIFTALATSNLIGILCARSLHYQFYAWFAWSPYLCY 354

Query: 402 KARLNFIASIIIVYAAHEYCWLVFPATEQSS 431
 +A I ++ EY W VFP+T+ SS

Sbjct: 355 QASFPAPIVIGLWMLQEYAWNVPSTKLSS 384
Arabidopsis thaliana

Score = 164 bits (415), Expect = 2e-39
 Identities = 131/391 (33%), Positives = 194/391 (49%), Gaps = 29/391 (7%)

Query: 42 LWLADSIIVIKVIIGTVSYTDIDFSSYMQQIFKIRQGEIDYSNIFGDTGPLVYPAGHVHAY 101
 L LAD+I++ +II V YT ID+ +YM Q+ GE DY N+ GDTGPLVYPAG ++ Y

Sbjct: 39 LILADAILVALIIAYVPYTKIDWDAYSQVSGFLGGERDYGNLKGDTGPLVYPAGFLYVY 98

Query: 102 SVLSWYSDGGEDVSFVQAFGWLYLGCLLLSISSYFFSGLGKIPVYFVLLVASKRLHSI 161
 S + + G +V Q FG LY+ L + + Y + + +P LL SKR+HSI

Sbjct: 99 SAVQNLTTGG--EVYPAQILFGVLYIVNLGIVLIYVKTDV--VPWWALSLLCLSKRIHSI 154

Query: 162 FVLRLFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVDAADTYSLAISVMNXXXXX 221
 FVLRLFNDC L+ A++ + +RK + + +S A+SVKMN

Sbjct: 155 FVLRLFNDCFAMTLLHASMALFL----YRKWHLGMLV-----FSGAVSVKMNVLLYA 202

Query: 222 XXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPLHYDDQANEIRSAYFRQAFDF 281
 N+I ++ F++ +Y AFD

Sbjct: 203 PTLLLLLLLKAM--NIIGVVSALAGAALAQILVGLPFLITYPV-----SYIANAFDL 251

Query: 282 SRQFLYKWTNVNRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341
 R F++ W+VN++F+ + F + F L H+ LV F + K+ G +G

Sbjct: 252 GRVFIHFWSVNFKFVPERVFSKEFAVCLLIAHLFLLVAFA-NYKWCKHEGGIIGFMRSR 310

Query: 342 IFKFWKP-TLSPTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWYAFSLPYLL 400
 F P +LS +++ + + V T M N IG++FARSLHYQF SWY +SLPYLL

Sbjct: 311 HFFLTLPSSLSFSDVSASRIITKEHVVTAMFVGNFIGIVFARSLHYQFYSWYFYSPLPYLL 370

Query: 401 YKARLNFIASIIIVYAAHEYCWLVFPATEQSS 431
 ++ +I++ E CW V+P+T SS

Sbjct: 371 WRTPFPTWLRLLIMFLGIELCWNVPSTPSSS 401

FIG. 19-3

K. lactis ALG3

TTTGTTTACAAGCTGATACCAACGAACATGAATACACCGGCAGGTTTACT
GAAGATTGGCAAAGCTAACCTTTTACATCCTTTTACCGATGCTGTATTCAG
TGCGATGAGAGTAAACGCAGAACAAATTGCATACATTTTACTTGTTACCA
ATTACATTGGAGTACTATTTGCTCGATCATTACACTACCAATTCCTATCTT
GGTACCATTGGACGTTACCAGTACTATTGAATTGGGCCAATGTTCCGTATC
CGCTATGTGTGCTATGGTACCTAACACATGAGTGGTGCTGGAACAGCTAT
CCGCCAAACGCTACTGCATCCACACTGCTACACGCGTGTAACACATACTG
TTATTGGCTGTATTCTTAAGAGGACCCGCAAACCTCGAAAAGTGGTGATAA
CGAAACAACACACGAGAAAGCTGAG

K. lactis Alg3p

FVYKLIPTNMNTPAGLLKIGKANLLHPFTDAVFSAMRVNAEQLAYILLVTNYI
GVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLCVLWYLTHEWCWNSYPP
NATASTLLHACNTYCYWLYSZEDPQTRKVITKQHTRKL

FIG. 20

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K. lactis ALG3 BLAST

Score E (bits) Value
 Sequences producing significant alignments:

qi 586444 sp P38179 ALG3 YEAST	Dolichyl-P-Man:Man(5)GlcNAc(...)	125	1e-28
qi 984725 gb AAA75352.1	ORF 1	94	4e-19
qi 16226531 gb AAL16193.1 AF428424.1	At2g47760/F17A22.15 [A...	72	1e-12
qi 25367230 pir B84919	Not56-like protein [imported] - Ara...	72	1e-12
qi 21292031 gb EAA04176.1	agCP3388 [Anopheles gambiae str....	69	2e-11
qi 20892051 ref XP_148657.1	similar to Lethal(2)neighbour ...	65	2e-10

Alignments

S. cerevisiae

Score = 125 bits (314), Expect = 1e-28
 Identities = 60/120 (50%), Positives = 83/120 (69%), Gaps = 1/120 (0%)
 Frame = +3

Query: 66 ANLLHPFT-DAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWA 242
 ++L HP +AV +A A+ I ++L+ +N+IGVLF+RSLHYQFLSWYHWTLP+L+ W+
 Sbjct: 332 SSLCHPLRKNVNLNANP--AKTIPFVLIASNFIVGVLFSRSLHYQFLSWYHWTLPILIFWS 389

Query: 243 NVYPYPLCVLWYLTHEWCWNSYPPNATASTLLHACNTYCYWLYS*EDPQTRKVVITKQHTR 422
 +P+ + +WY+ HEWCWNSYPPN+ ASTLL A NT L + + V + K H R
 Sbjct: 390 GMPFFVGPIWYVLHEWCWNSYPPNSQASTLLALNTVLLLLLA-LTQLSGSVALAKSHLR 448

A. thaliana

Score = 72.0 bits (175), Expect = 1e-12
 Identities = 42/107 (39%), Positives = 57/107 (53%), Gaps = 3/107 (2%)
 Frame = +3

Query: 84 FTDVAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWANVYPYPLC 263
 F+D S + + E + + V N+IG++FARSLHYQF SWY ++LP LL P L
 Sbjct: 322 FSDVSASRI-ITKEHVVTAMFVGNFIVGVLFSRSLHYQFYSWYFYSLPYLLWRTPFPTWLR 380

Query: 264 VLWYLTHEWCWNSYPPNATASTL---LHACNTYCYWLYS*EDPQTRK 395
 ++ +L E CWN YP ++S L LH WL DP K
 Sbjct: 381 LIMFLGIELCWNVYPSTPSSSGLLLCLHLIILVGLWLAPSVDPYQLK 427

FIG. 21

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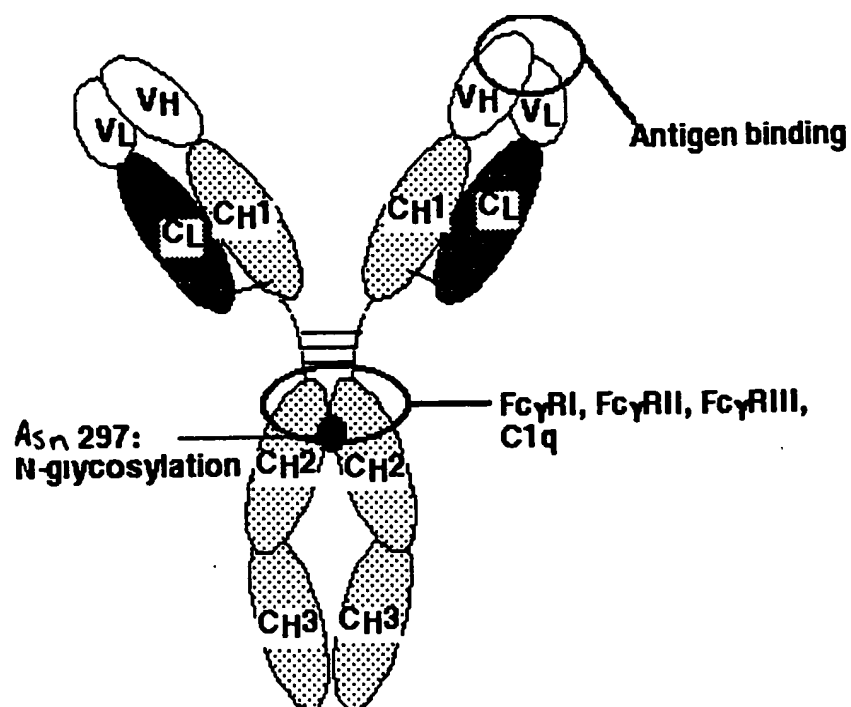


FIG. 22

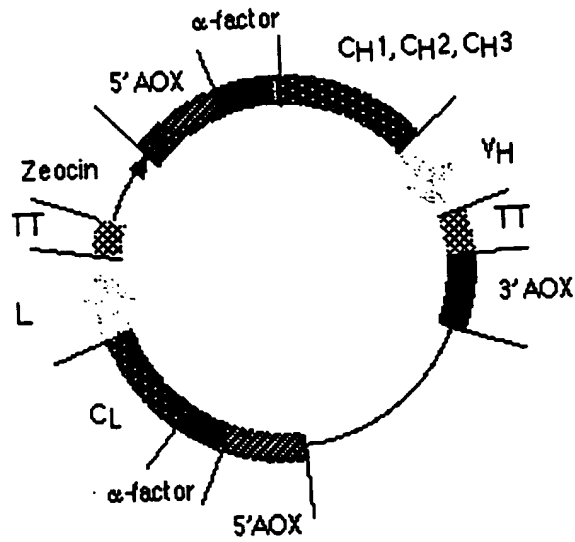


FIG. 23

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>gi|6754685|ref|NM_010795.1| Mus musculus mannoside acetyl
glucosaminyltransferase 3 (Mgat3), mRNA

ATGAAGATGAGACGCTACAAGCTCTTTCTCATGTTCTGTATGGCTGGCCTGTGCCTCATATCCTTCCTGC
ACTTCTTTAAGACCTTATCCTATGTACCTTCCCGAGAGAACTGGCCTCCCTCAGCCCTAACCTCGTATC
CAGCTTCTTCTGGAACAATGCCCCGTGCTACTCCCCAGGCCAGTCCGGAGCCGGGTGGCCCCGACCTATTG
CGGACACCCCTCTACTCCCACTCTCCCTGCTCCAGCCACTGTCCCGAGCAAGGCCACAGAGGAACTGC
ACCGGGTGGACTTCGTGTTGCCGGAGGACACCACGGAGTATTTGTGCGCACCAAAGCTGGTGGTGTGTG
CTTCAAACCAGGTACCAGGATGCTGGAGAACTTCGCCAGGGCGGACAGAGGAGAAGCCCCGAAGTGTCT
GAGGGCTCCTCAGCCCGGGGACCTGCTCGGAGGCCCATGAGGCACGTGTTGAGTACGCGGGAGCGCCTGG
GCAGCCGGGGCACTAGGCGCAAGTGGGTTGAGTGTGTGTGCTGCCAGGCTGGCACGGGGCCAGTTGCCG
GGTGGCCACGGTGGTGAGTATTCCAACCTGCCACCAAGGAACGCCTGGTACCCAGGGAGGTACCGAGG
CGGGTTATCAACGCCATCAACATCAACCAGAGTTCGACCTGCTGGATGTGCGCTTCATGAGCTGGGAG
ATGTTGTGGACGCCTTCGTGGTCTGTGAATCTAATTTACCGCCTACGGGGAGCCTCGGCCGCTCAAGTT
CCGAGAGATGCTGACCAATGGCACCTTCGAGTACATCCGCCACAAGGTGCTCTATGTCTTCTGGACCAT
TTCCACCTGGTGGCCGTGAGGACGGCTGGATTGCGGATGACTACCTGCGCACCTTCCTACCCAGGATG
GCGTCTCCCGCCTGCGCAACCTGCGGCCGATGACGTCTTTATCATCGACGATGCGGACGAGATCCCTGC
GCGTGATGGTGTGCTGTTCTCAAACCTCTACGATGGCTGGACAGAGCCCTTCGCCTTCCACATGCGGAAG
TCCTGTATGGTTTCTTCTGGAAGCAGCCGGGCACACTGGAGGTGGTGTGAGGCTGCACCATGGACATGC
TGCAGGCCGTGTATGGGCTGGATGGCATCCGCTGCGCGCCGCCAGTACTACACCATGCCCAACTTCCG
GCAGTATGAGAACCACCGCCGACATCCTAGTGACGTGGTCTCTCGGCAGCCCCCTGCACTTCGCGGGC
TGGCATTGCTCCTGGTGCTTCACACCGAGGGCATCTACTTTAAACTCGTGTGAGCCAGAAATGGCGACT
TCCCCCGCTGGGGTGACTATGAGGACAAGAGGGACCTCAATTACATCCGCAGCTTGATCCGCACTGGGGG
ATGGTTTCGACGGAACGCAGCAGGAGTACCCTCCTGCGGACCCCACTGAGCACATGTATGCTCCTAAATAC
CTGCTCAAGAACTATGACCAGTTCGCTACTTGCTGGAAAATCCCTACCGGGAGCCCAAGAGCACTGTAG
AGGGTGGGCGCCAGAACCAGGGCTCAGATGGAAGGCCATCTGCTGTGAGGGGCAAGTTGGATACAGTGA
GGGCTAG

>gi|2117717|pir||JC4362 beta-1,4-mannosyl-glycoprotein 4-beta-N-
acetylglucosaminyltransferase (EC 2.4.1.144) III - mouse
MRRYKLFMFCMAGLCLISFLHFFKTL SYVTFPRELASLSPNLISSFFWNNAPVTPQASPEPGDPDLLRT
PLYSHSPLLQPLSPSKATEELHRVDFVLPEDTTEYFVRTKAGGVCFKPGTRMLEKPSGRTEEKTEVSEG
SSARGPARRPMRHLSSRERLGSRGTRRKWVECCLPGWHGPGVPTTVQYSNLP TKERLVPREVPRRV
INAININHEFDLLDVRFHLDVDFVVDASNFTAYGEPRPLKFREMLTNGTFEYIRHKVLYVFLDHFP
PGRQDGIADYLRFTLQDGVSRRLRNLRPDDVFIIDDADEIPARDGVLFLKLYDGTWTEPF AFHMRKSL
YGF FWKQPGTLEVVSGCTMDMLQAVYGLDGIRLRRRQYYT MPNFRQYENRTGHILVQWSLGSPLHFAGWH
CSWCFTPEGIYFKLVSAQNGDFPRWGDYEDKRD LNYIRSLIRTGGWFDGTQOEYPPADPSEHMYAPKYL
KNYDQFRYLLNPYREPKSTVEGGRQNQSDGRSSAVRGKLDTAEG

FIG. 24

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Fig. 25

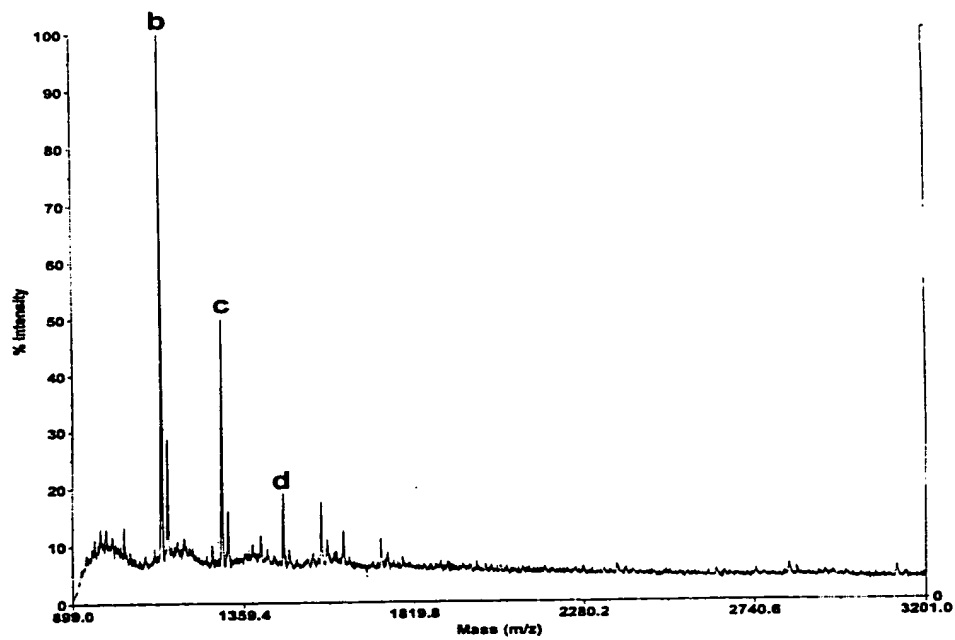
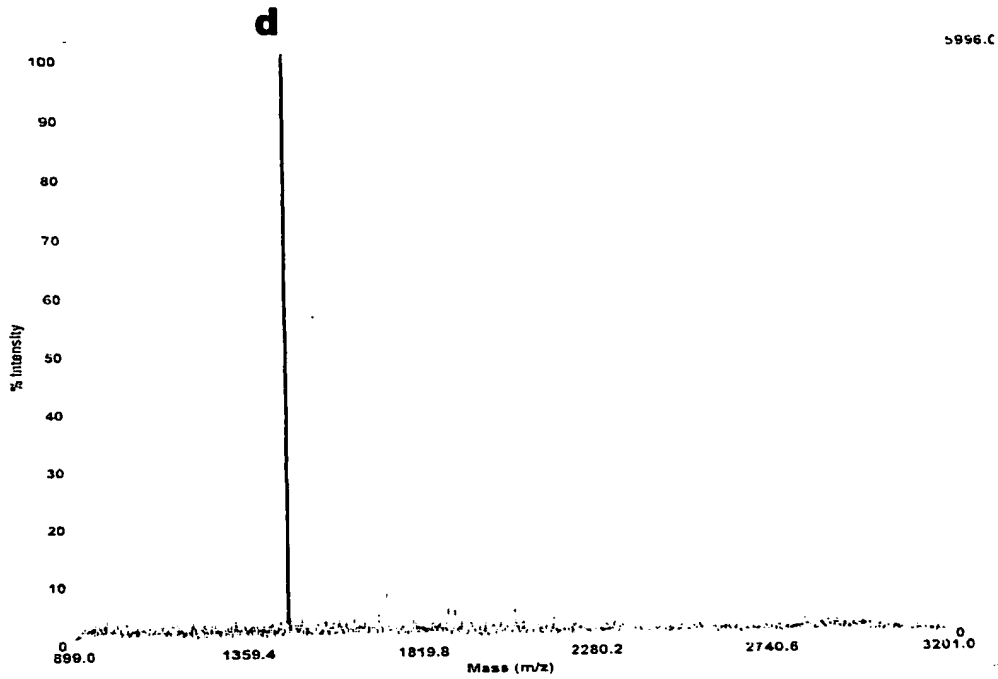
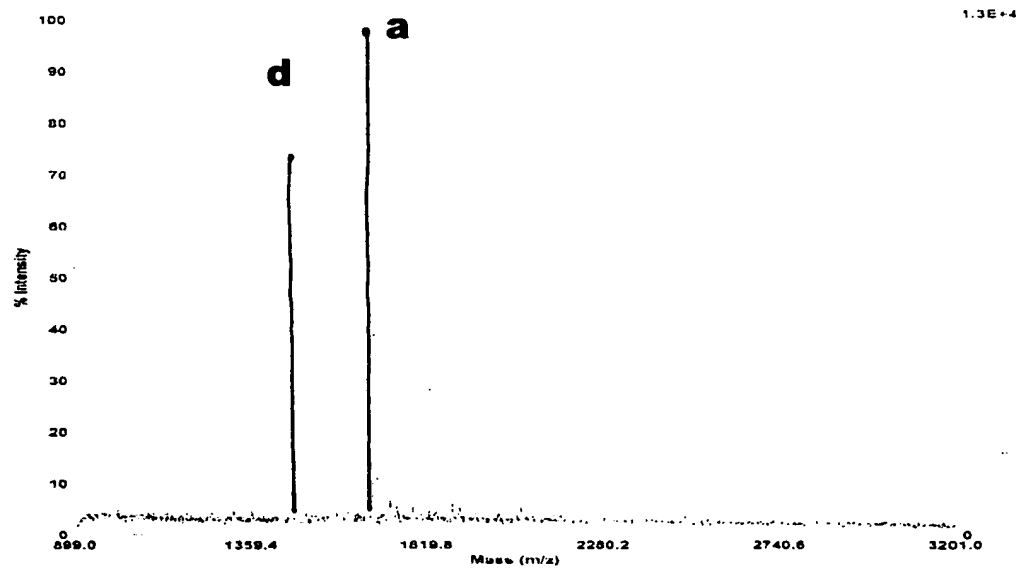
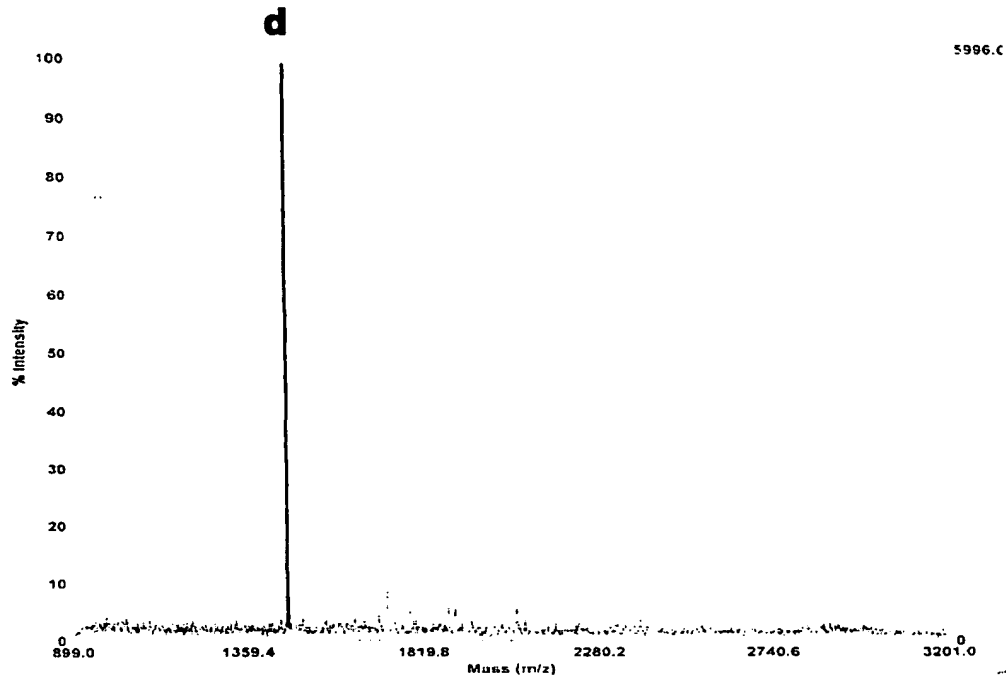
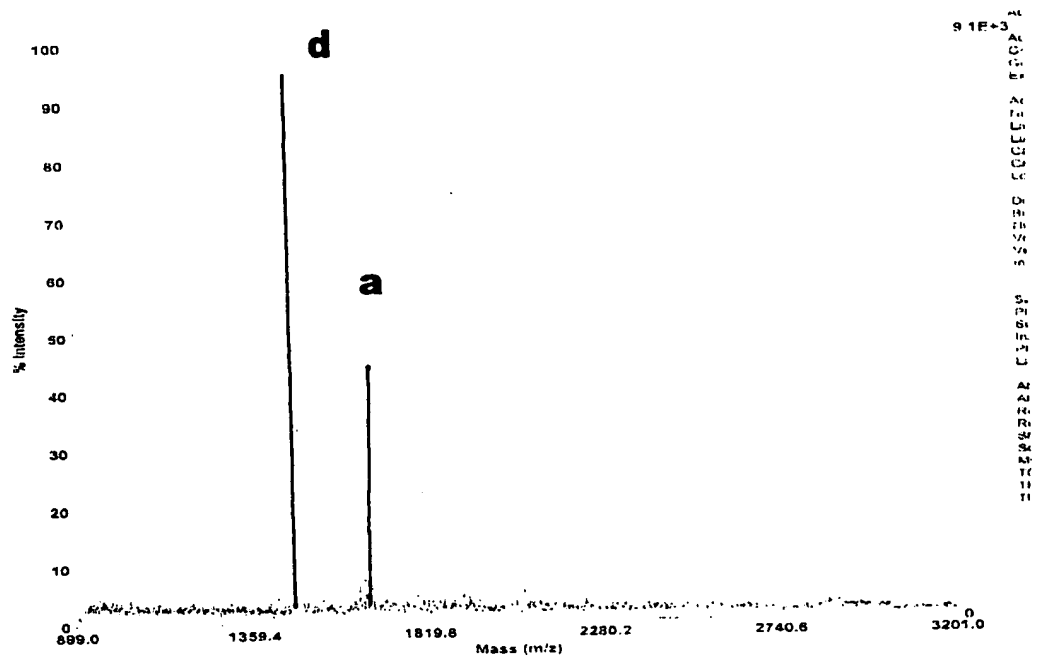
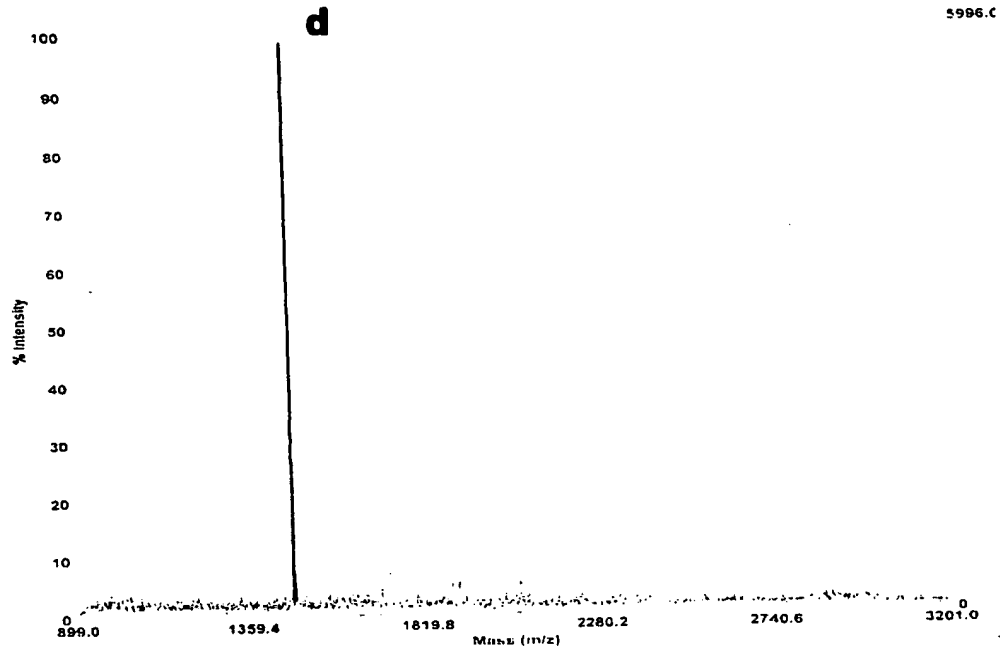


Fig. 26



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Fig. 27



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Fig. 28

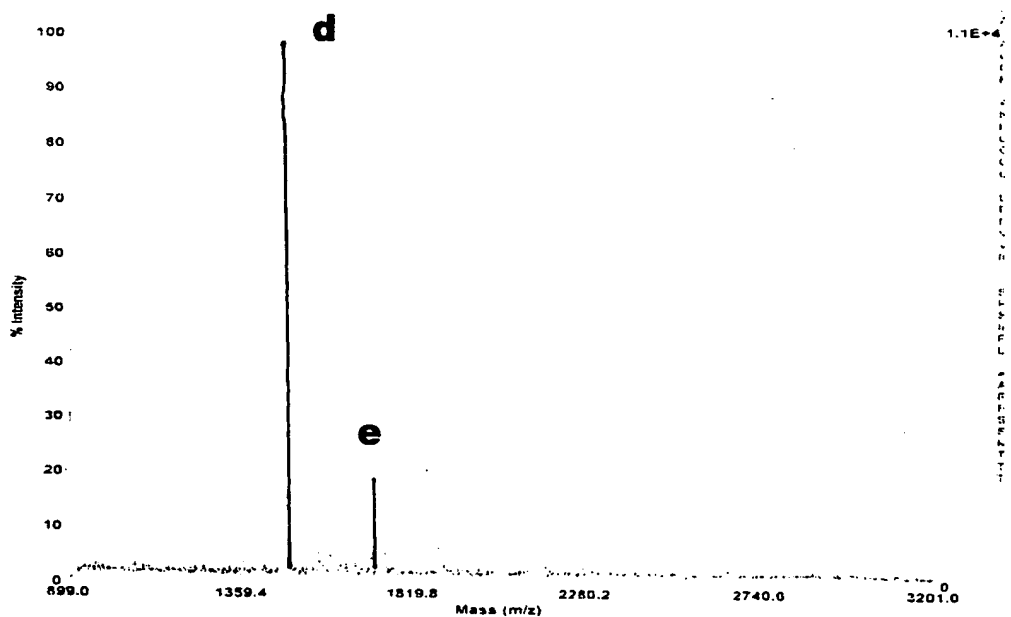
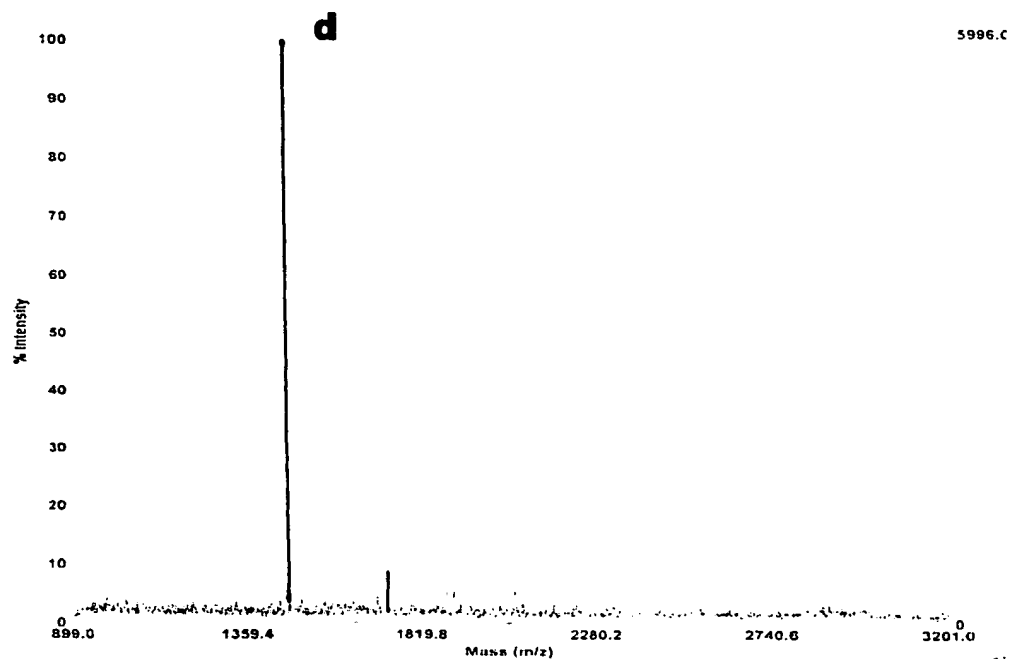


Fig. 29

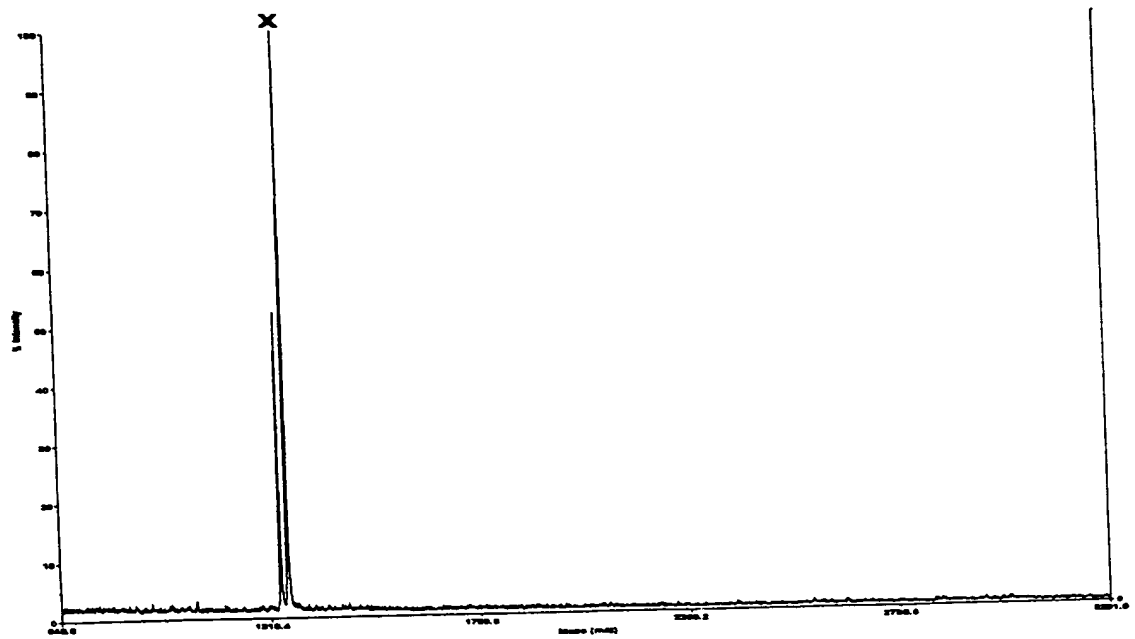
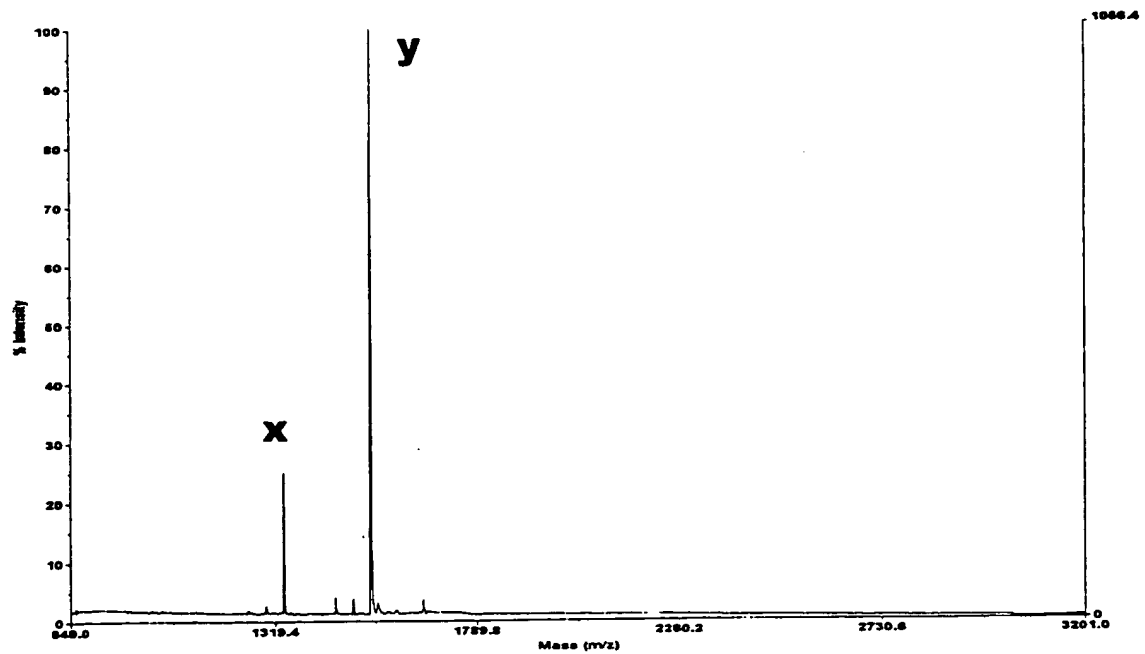


Fig. 30



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Fig. 31

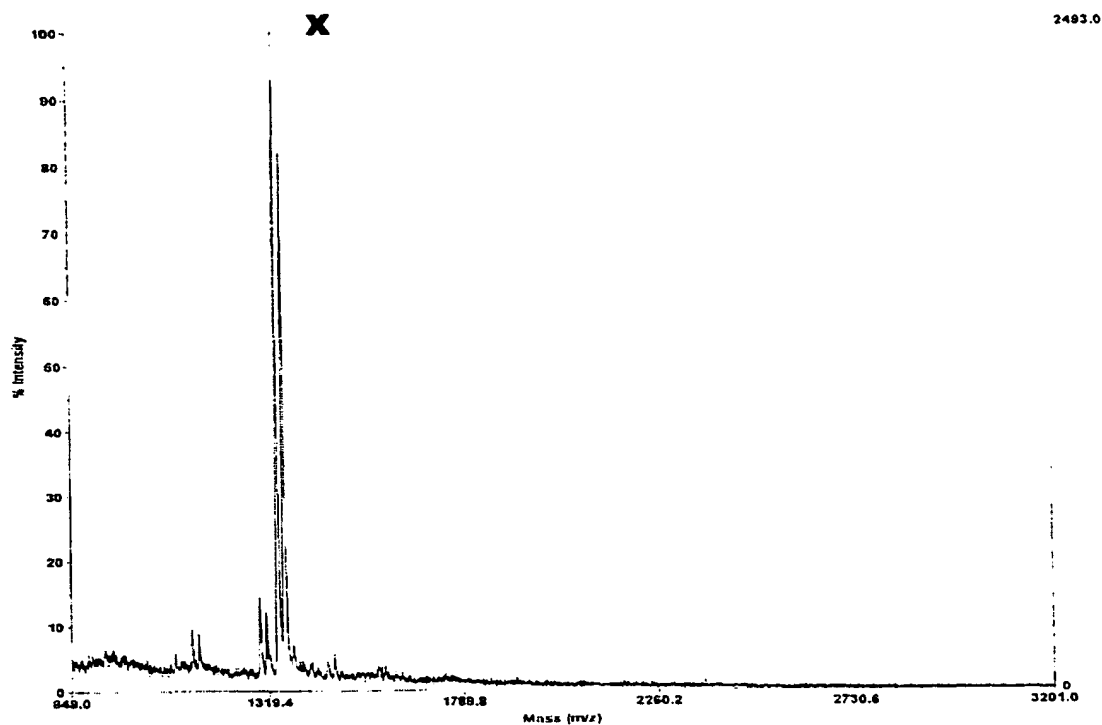
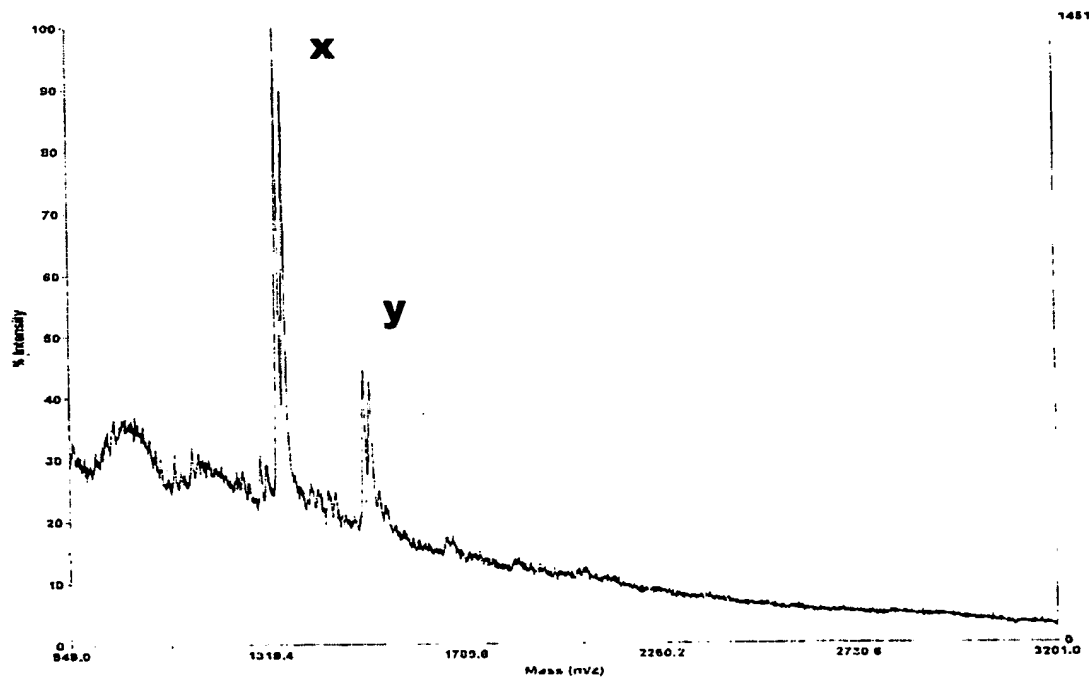
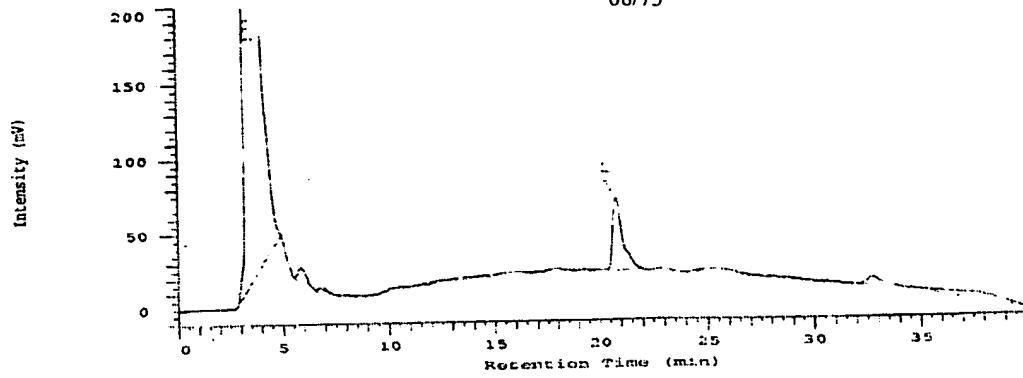


Fig. 32

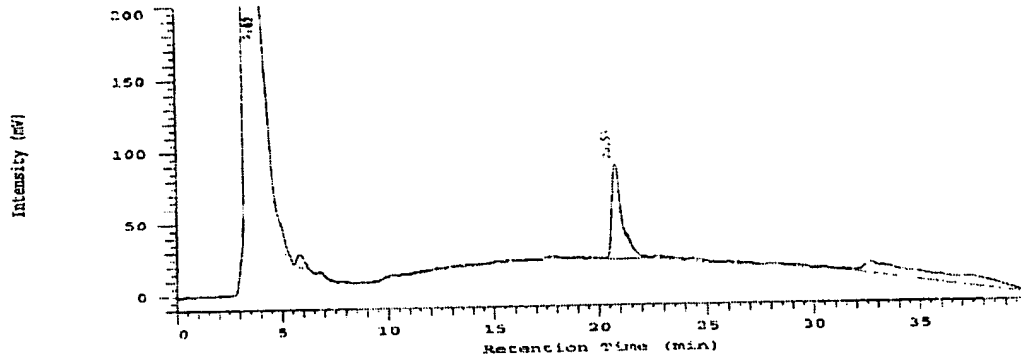


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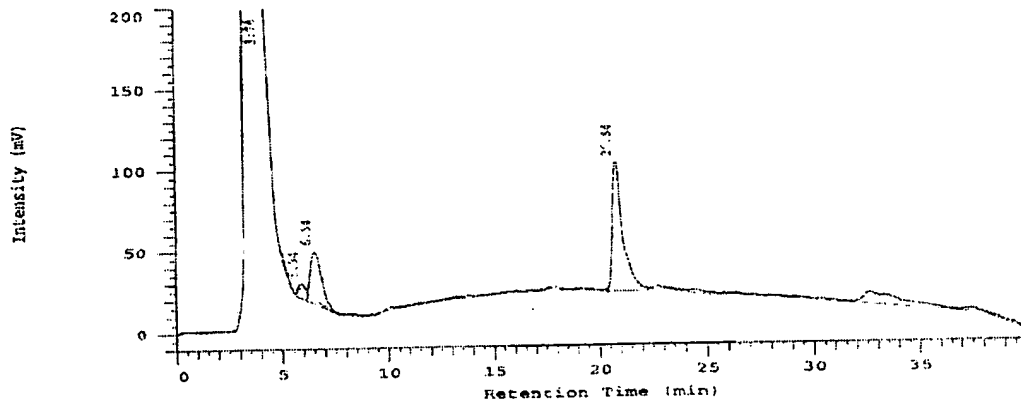
A



B



C



D

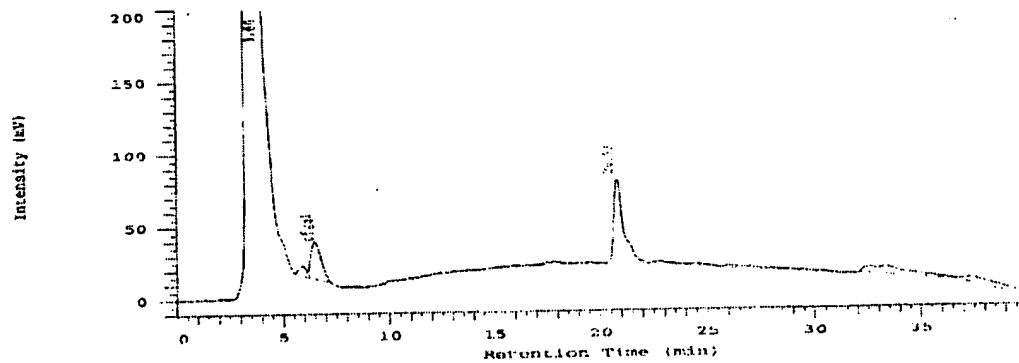
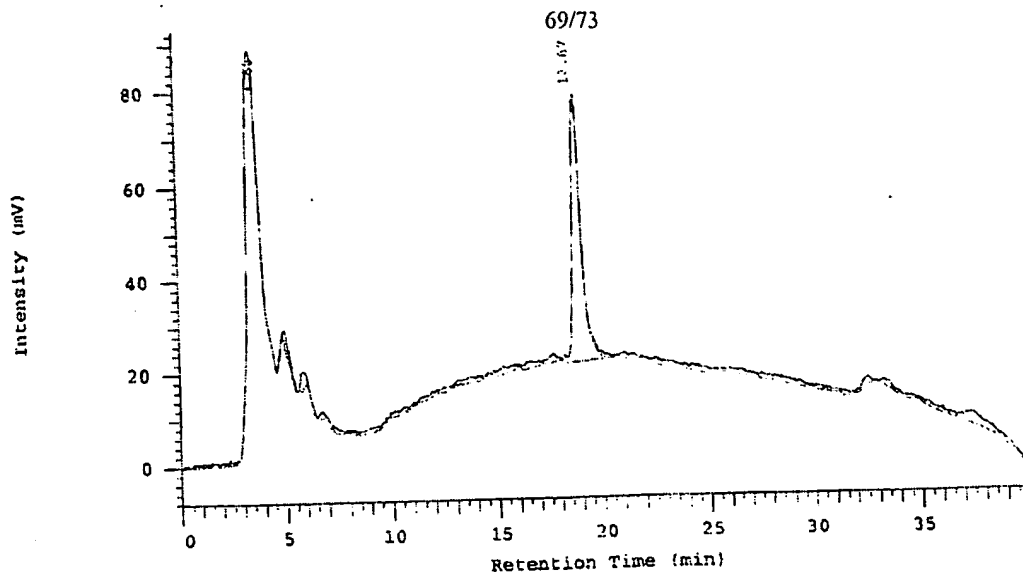
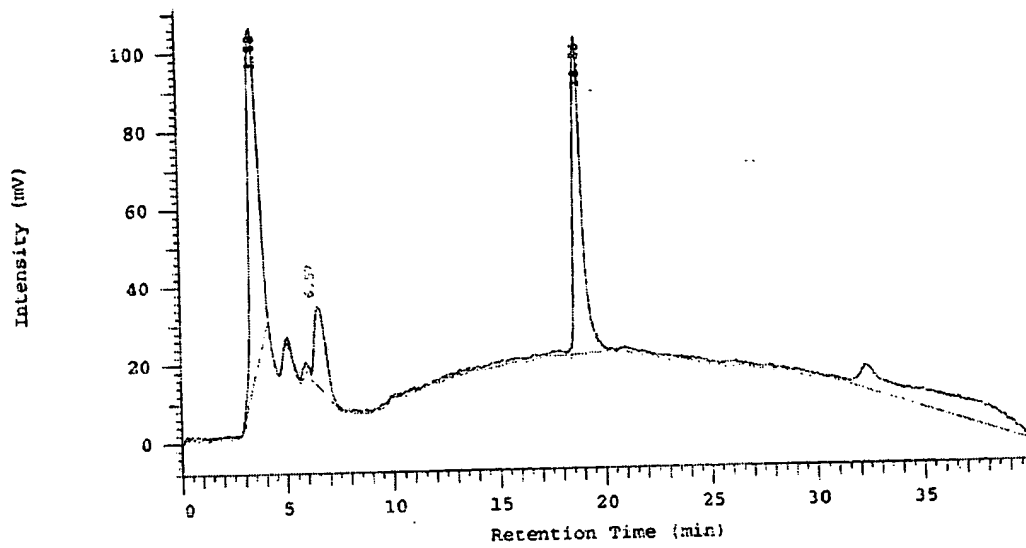


Fig. 33

A



B



C

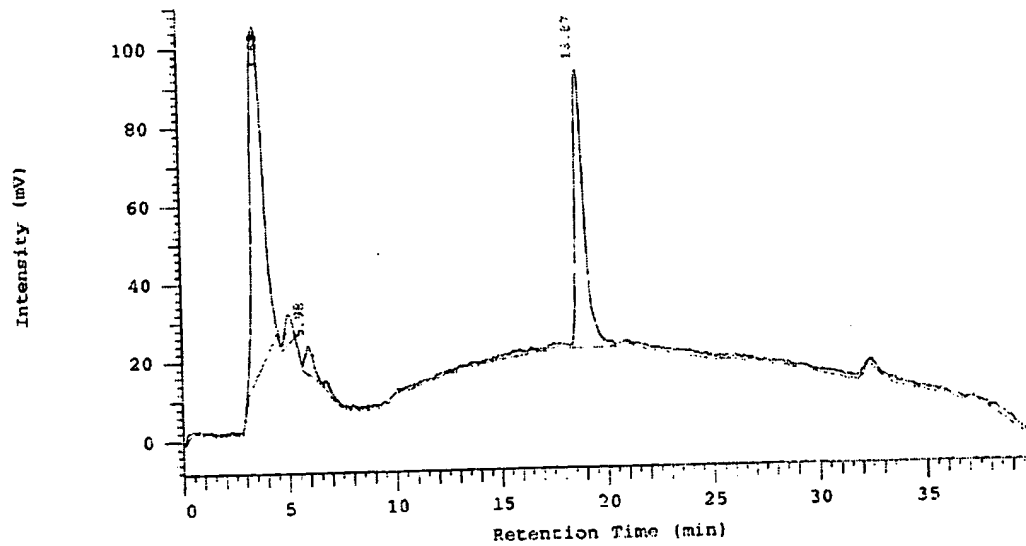


Fig. 34

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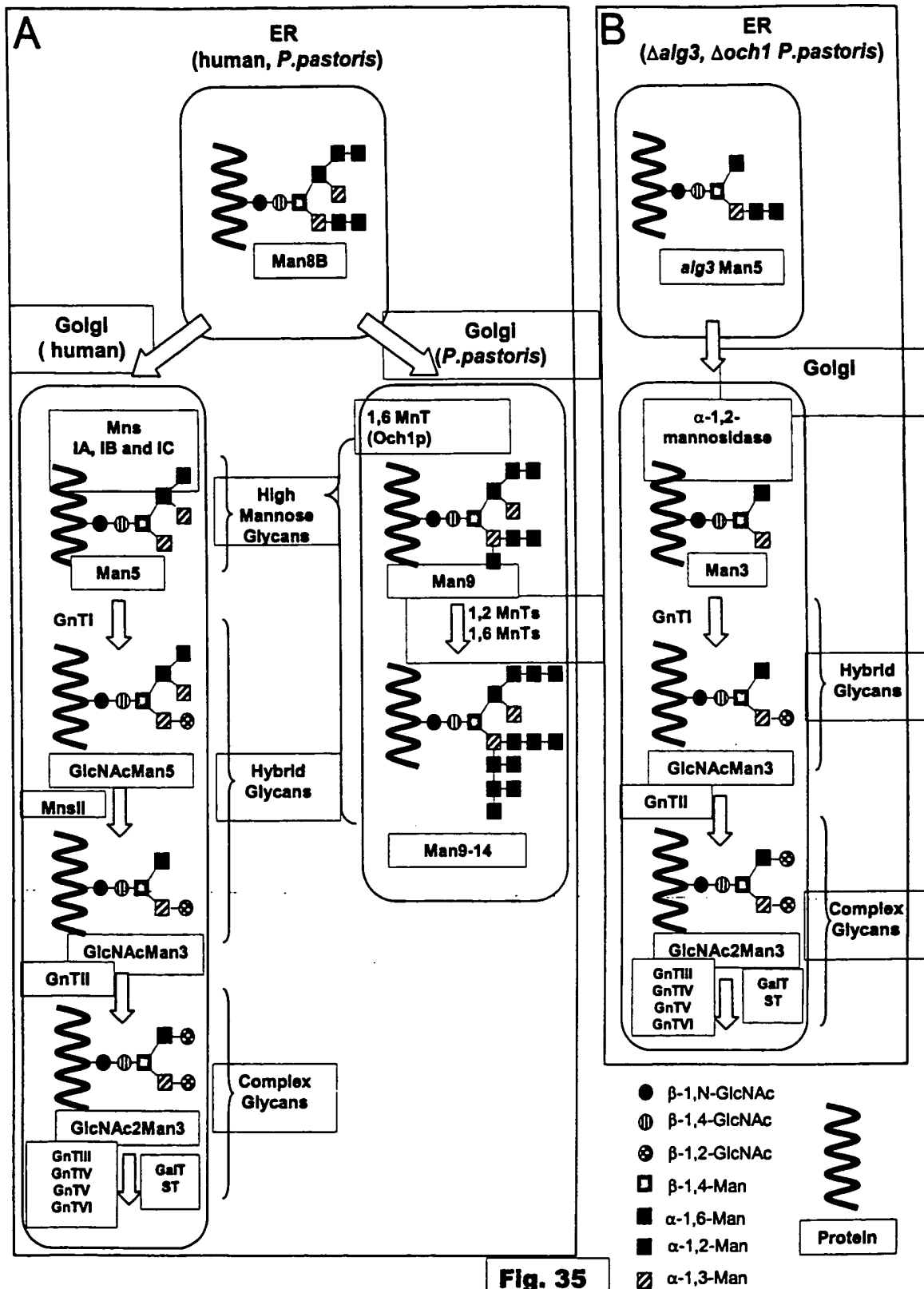


Fig. 36

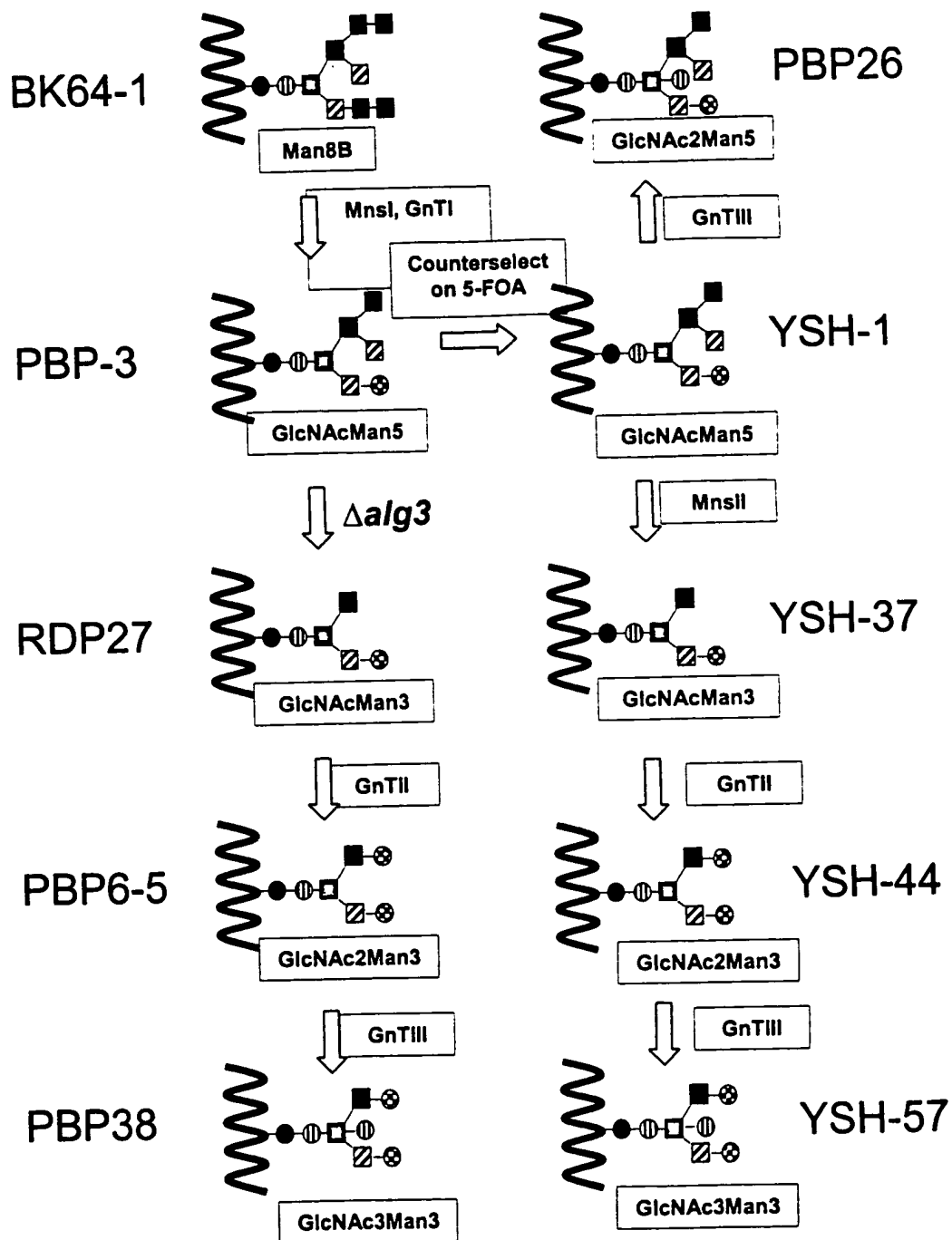


Fig. 37

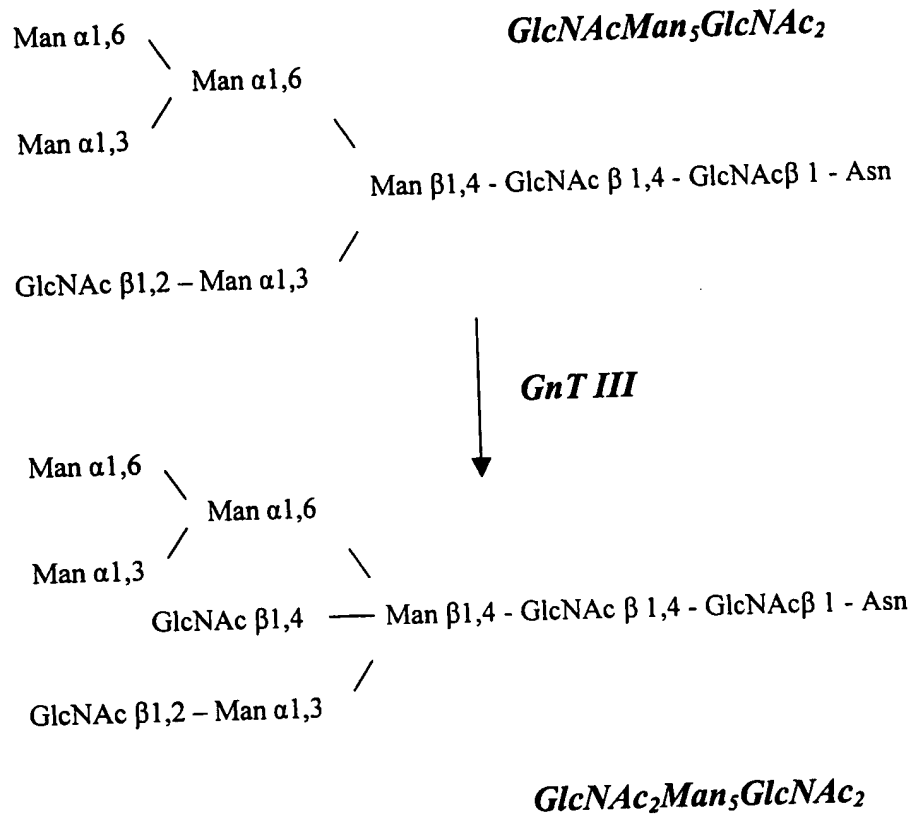


Fig. 38

